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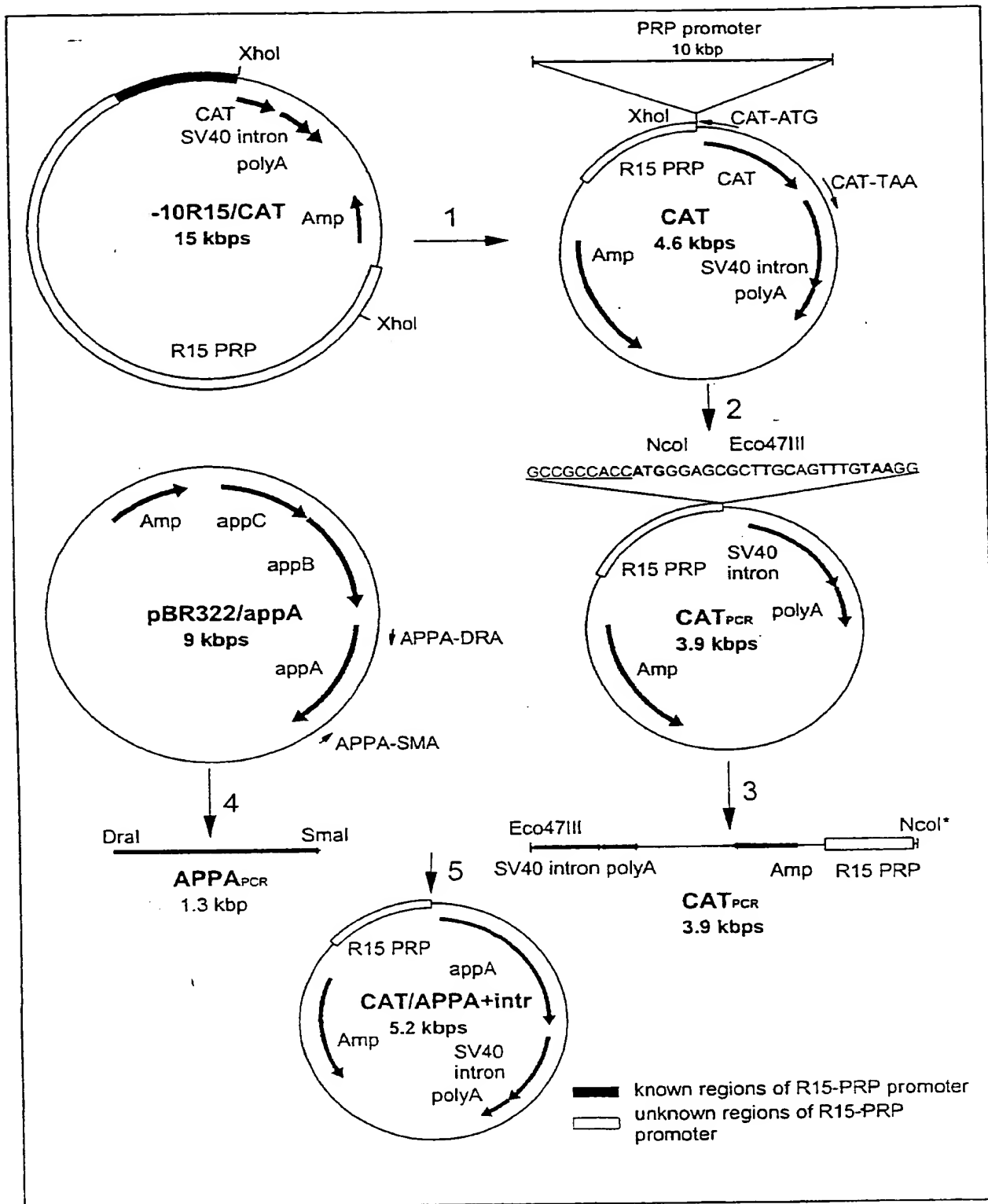
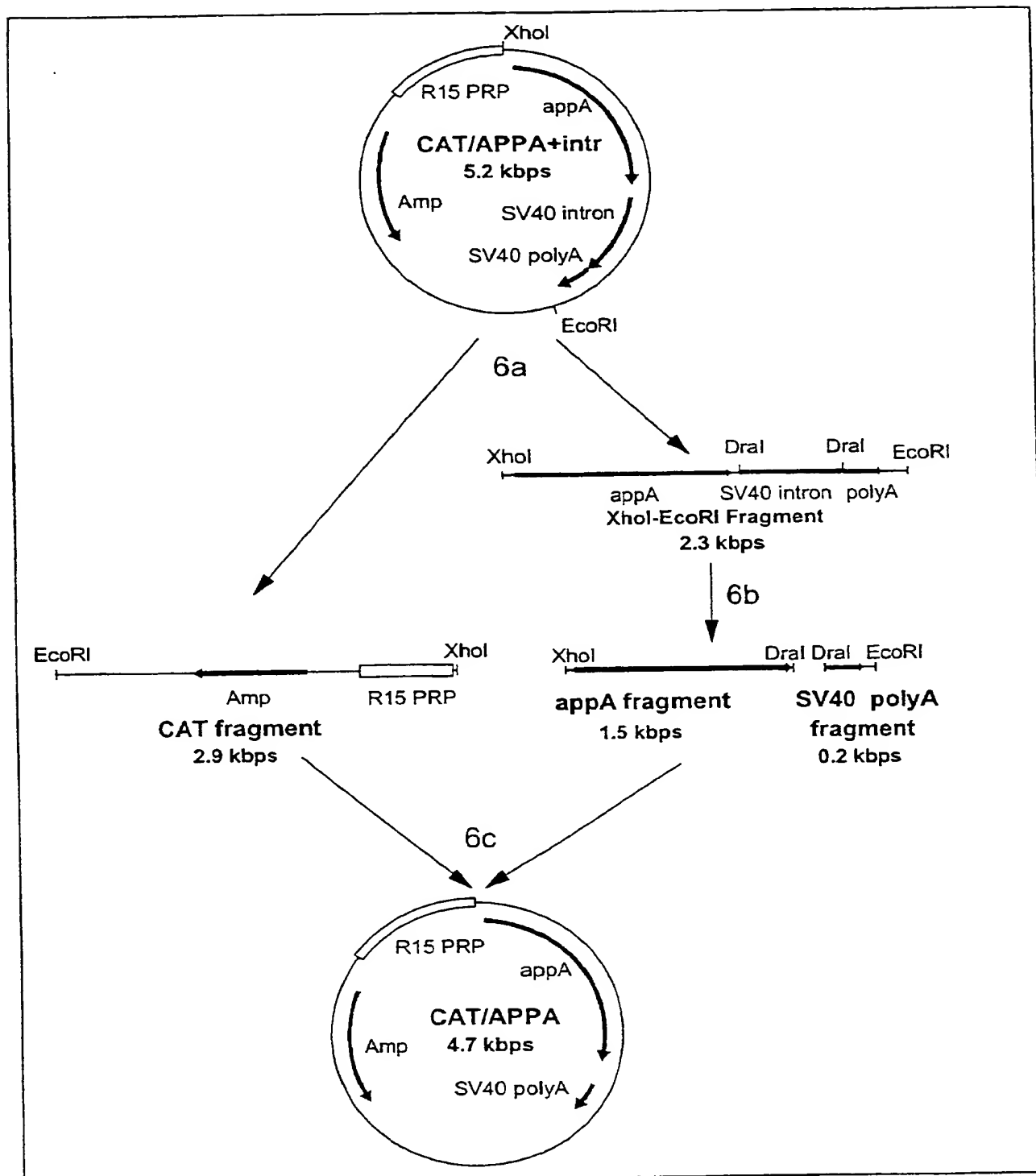


Figure 1

**Figure 1 (continued)**

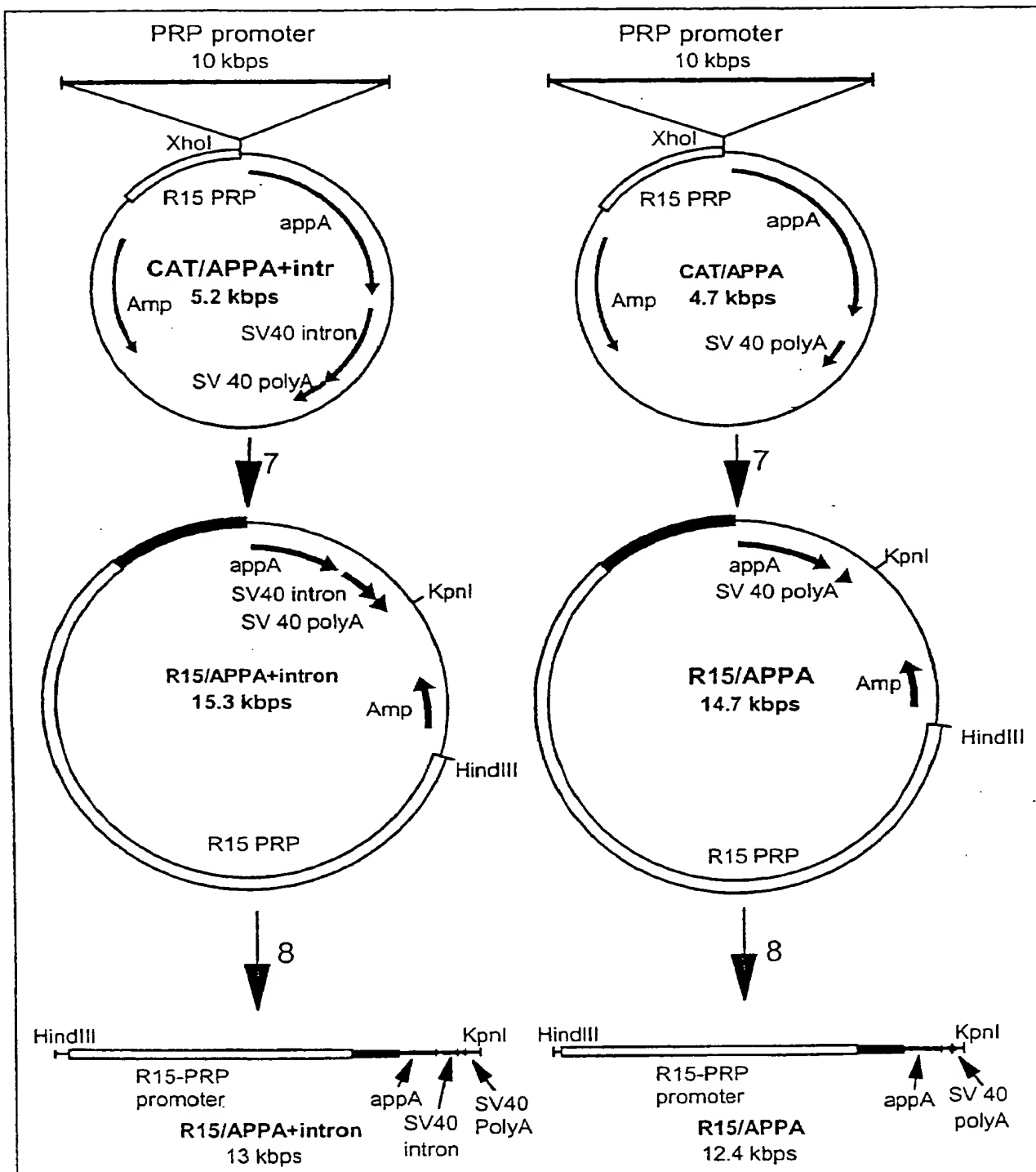
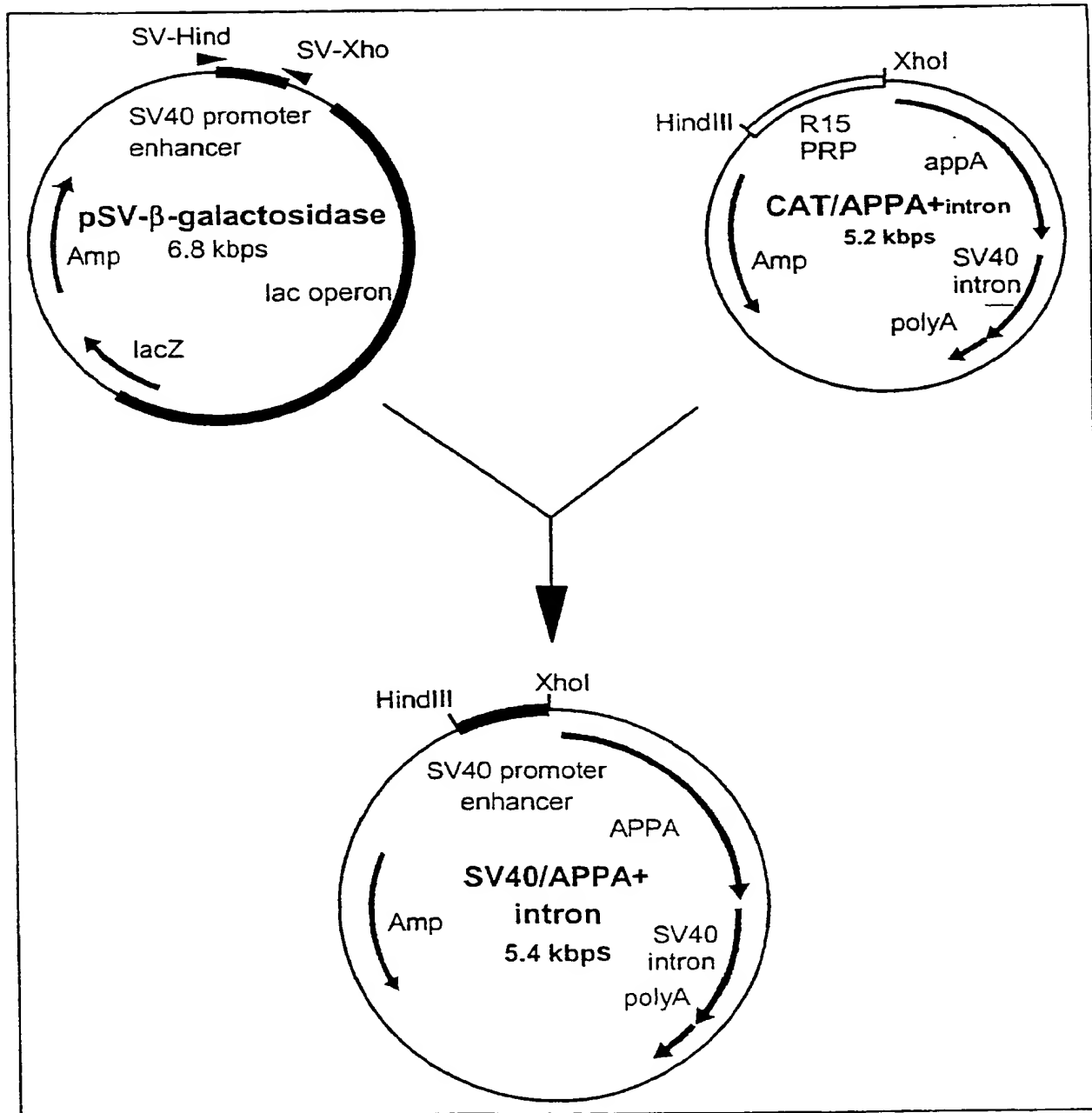
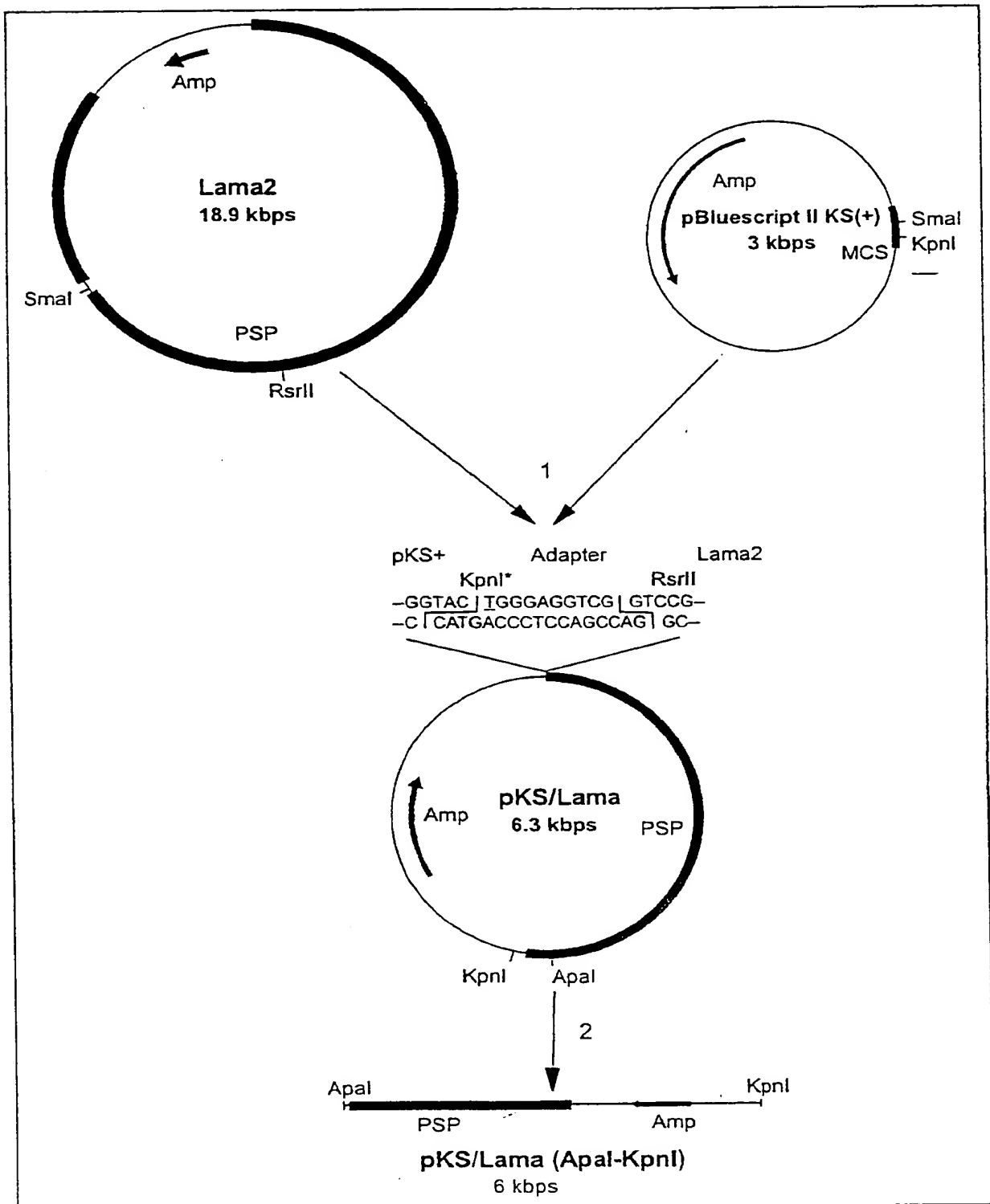


Figure 1 (continued)

**Figure 2**

**Figure 3**

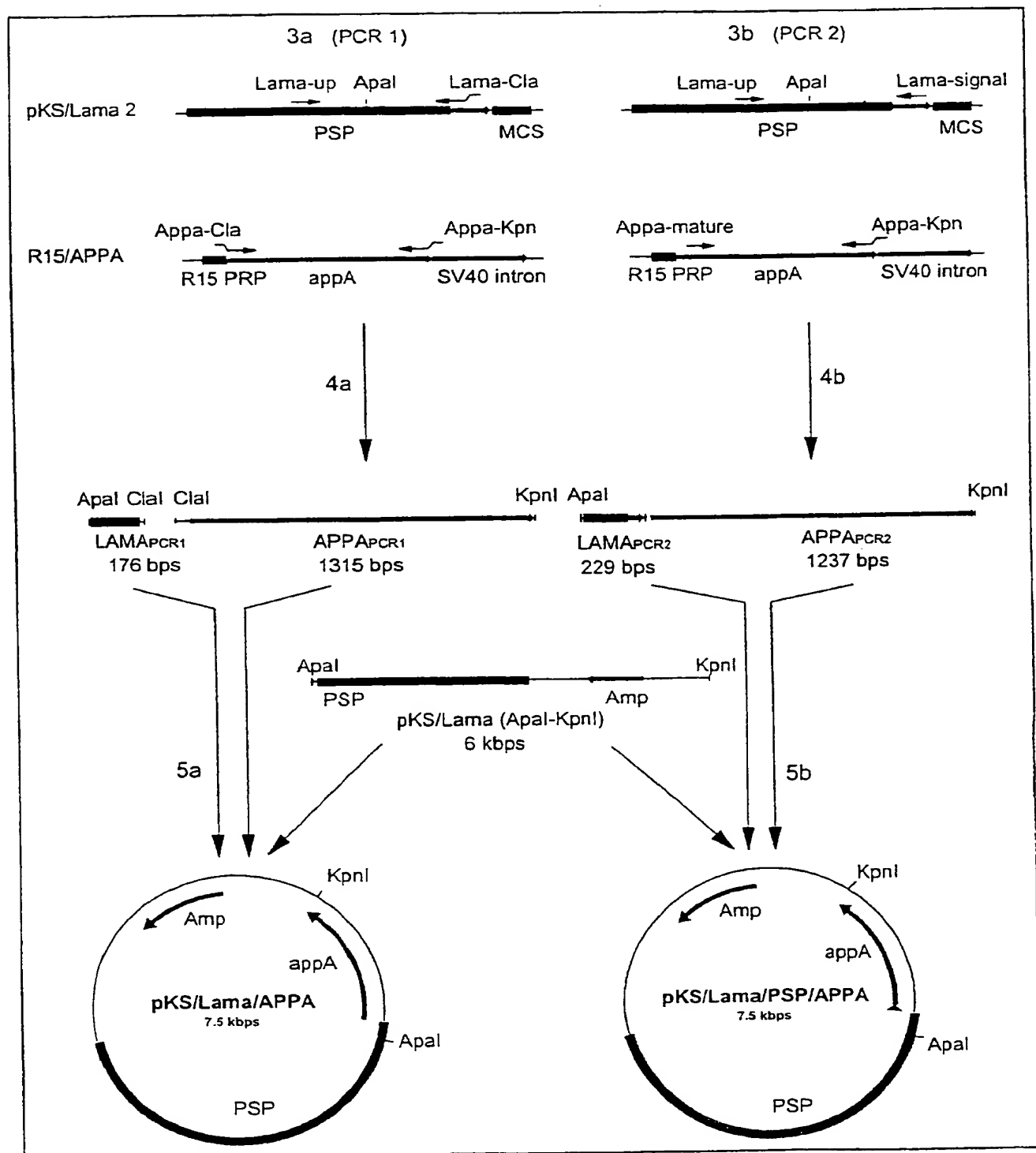


Figure 3 (continued)

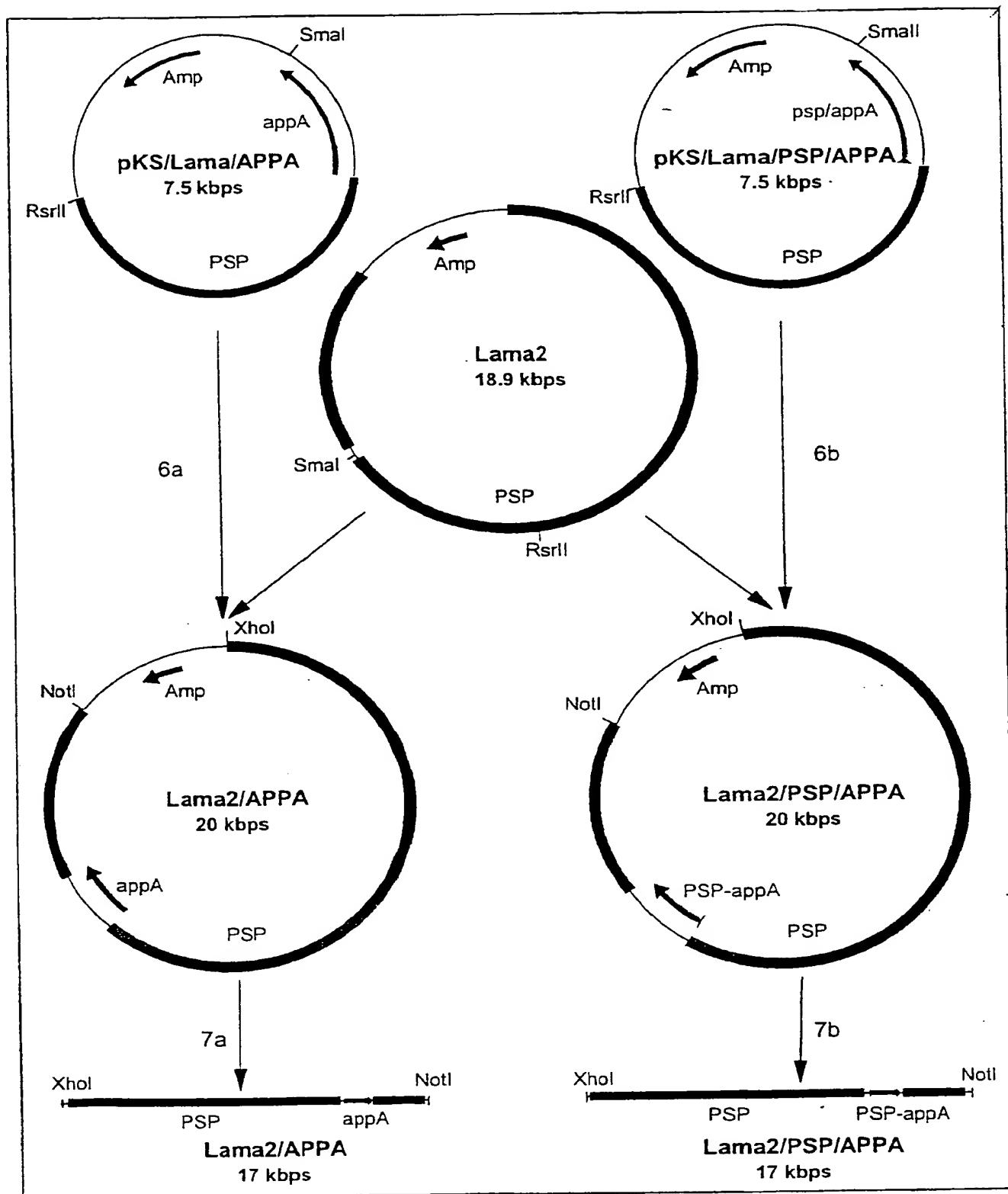


Figure 3 (continued)

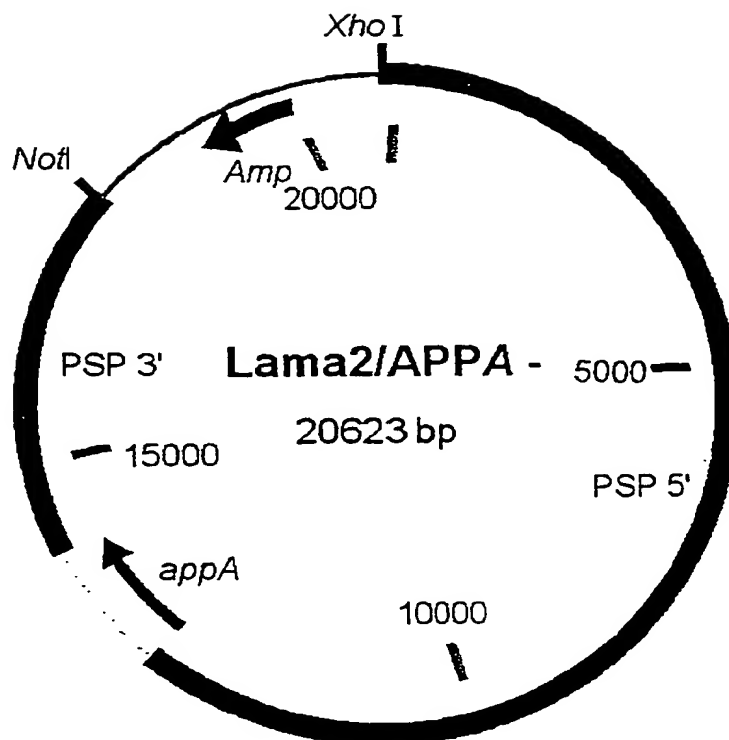


Figure 4. Schematic diagram of the Lama2/APPa construct.

Figure 5. The nucleic acid sequence of the Lama2/APPA plasmid (SEQ ID NO: 1)

LOCUS Lama-appA 20623 bp DNA CIRCULAR SYN 17-JAN-2000
 DEFINITION Lama 2/APPA transgenic construct
 ACCESSION Lama 2-appA,
 KEYWORDS parotid secretory protein; acid glucose-1-phosphatase; appA
 gene;
 periplasmic phosphoanhydride phosphohydrolase; artificial
 sequence;
 cloning vector
 REFERENCE 1 (bases 1 to 20623)
 AUTHORS Golovan, S., Forsberg, C.W., Phillips, J.
 JOURNAL Unpublished.
 FEATURES
 DEFINITION M. musculus Psp gene for parotid secretory protein.
 ACCESSION X68699
 VERSION X68699.1 GI:53809
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 3777 to 5332;)
 AUTHORS Svendsen, P., Laursen, J., Krogh-Pedersen, H. and Hjorth, J. P.
 TITLE Novel salivary gland specific binding elements located in the PSP
 proximal enhancer core
 JOURNAL Nucleic Acids Res. 26 (11), 2761-2770 (1998)
 MEDLINE 98256451
 REFERENCE 2 (bases 7147 to 12653; 13952 to 17731)
 AUTHORS Mikkelsen, T. R.
 TITLE Direct Submission
 JOURNAL Submitted (07-OCT-1992) T. R. Mikkelsen, Department of Molecular
 Biology, University of Aarhus, CF Mollers Alle 130, 8000
 Aarhus, DENMARK
 REFERENCE 3 (bases 7147 to 12653; 13952 to 17731)
 AUTHORS Laursen J, Hjorth JP
 TITLE A cassette for high-level expression in the mouse salivary glands.
 JOURNAL Gene 1997 Oct 1;198(1-2):367-72
 MEDLINE 9370303

FEATURES Location/Qualifiers
 source 1.to 12653; 13952 to 17731
 /organism="Mus musculus"
 /strain="C3H/As"
 /db_xref="taxon:10090"
 /chromosome="2"
 /map="Estimate: 69 cM from centromere"
 /clone="Lambda YP1, Lambda YP3, Lambda YP7"
 /clone_lib="Lambda-PHAGE (Lambda L47.1)"
 /germline
 /note="Allele: b"
 misc_feature 3777-5332
 /gene="PSP"
 /function="salivary gland specific positive acting
 regulatory region"
 enhancer 7147..8724
 /evidence=experimental
 exon 11778..11824
 /gene="Psp"
 /note="exon a"
 /number=1
 /evidence=experimental
 exon 12626.. 14190
 /gene="Psp"
 /note="exon b fused with exons h and i"
 misc_feature 12644-12652

Figure 5 (continued):

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                /function=" consensus sequence for initiation in higher
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misc_feature 13952-13965
                /function=" M13mp18 polylinker"

DEFINITION  E. coli periplasmic phosphoanhydride phosphohydrolase (appA) gene,

ACCESSION  M58708 L03370 L03371 L03372 L03373 L03374 L03375
VERSION    M58708.1  GI:145283
SOURCE     Escherichia coli DNA.
ORGANISM   Escherichia coli
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Escherichia.

REFERENCE  1  (bases 12653..13951)
AUTHORS   Dassa,J., Marck,C. and Boquet,P.L.
TITLE     The complete nucleotide sequence of the Escherichia coli gene appA
            reveals significant homology between pH 2.5 acid phosphatase
            and glucose-1-phosphatase
JOURNAL    J. Bacteriol. 172 (9), 5497-5500 (1990)
MEDLINE    90368616

FEATURES             Location/Qualifiers
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                        /db_xref="taxon:562"
     sig_peptide         12653..12718
                        /gene="appA"
     CDS12653           13951
                        /gene="appA"
                        /standard_name="acid phosphatase/phytase"
                        /transl_table=11
                        /product="periplasmic phosphoanhydride phosphohydrolase"
                        /protein_id="AAA72086.1"
                        /db_xref="GI:145285"

/translation="MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAP
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                        /product="periplasmic phosphoanhydride phosphohydrolase"

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                        /note="created by site directed mutagenesis"
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                        /phenotype=" silent mutation "
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Figure 5 (continued):

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/phenotype=" silent mutation "

DEFINITION      pBluescript II KS(+) vector DNA,
ACCESSION        X52327
VERSION          X52327.1  GI:58061
KEYWORDS         artificial sequence; cloning vector; expression vector; vector.
SOURCE           synthetic construct.
ORGANISM         synthetic construct
                 artificial sequence.

REFERENCE        1      (bases 17732 to 20623)
AUTHORS          Thomas,E.A.
TITLE            Direct Submission
JOURNAL          Submitted (20-FEB-1990) Thomas E.A., Stratagene Cloning
                 Systems, 11099 North Torrey Pines Rd., La Jolla, CA 92037, USA

REFERENCE        2      (bases 17732 to 20623)
AUTHORS          Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.
TITLE            Lambda ZAP: a bacteriophage lambda expression vector with in
                 vivo excision properties
JOURNAL          Nucleic Acids Res. 16 (15), 7583-7600 (1988)
MEDLINE          88319944
REFERENCE        3      (bases 17732 to 20623)
AUTHORS          Altling-Mees,M.A. and Short,J.M.
TITLE            pBluescript II: gene mapping vectors
JOURNAL          Nucleic Acids Res. 17 (22), 9494 (1989)
MEDLINE          90067967
FEATURES         Location/Qualifiers
Source           17732 to 20623
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CDS              complement (18967..19827)
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BASE COUNT      5449 a    4847 c    4902 g    5424 t
ORIGIN

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121 TGTGTAACAA GTTCTCCAAA GGAGAGATAC AGATGAGTGC GTATAGGGTG GACCTGGCTG
181 CTGAGGAGAC ACCTGCATCT GACTAAGAAG AGCCACGGTG TTAGTTGAAT GGTGTGGAGT
241 AGGGTGGTTC TGTGGGACAG TAGAAAATCG AGAGGCATGT GCCGTTAGT GAACCTGATGG
301 AAGCTACCCC AAACGACAGA GATTGTCACT CAGGCCAATC CGTTTCGAGT TTGATGGGCA
361 GCCGGACAGT GAGACAGACA CACCTACTCA GTTGGAGGAA GGATGAGAAC AATGGCCAGC
421 AGGGATTGAG AGACCCTGAC AGGCGCAAGG CCCTAACACA CACACCTACC ACCTCACTG
481 ACAAAGCTGC CAAAGACCAA AGACTTGTTC TCCATTAGAA ATGACAGCTG GCTTGACCCG
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661 TTAAAGTAGG GTAAAGTACT CTTTAAAAAT GGGTCCTAGA TATTTTTTCC TTAACTCAA
721 GTCTCTTACT GTTTAAATGA TTTTATTTT GTTTAATATG GAGGAAAAAG AAGCGTAAAT
781 GGACAATATA TATTTAGAGA AAGATGGTTA GCTGTCAGAA AAATATGCAA ATCAAAATCA
841 CACCAAGACT GCAGCACACC CCTGTCAGAT GGCTGTGATC AAGAAAATAA ATGACAATGA
901 GTGGTGGTGA AGATGTACTA AAGGGAAACA CACACACACA CACACACACA CACACACACA
961 CACACTGGAG CAACCACTGT GGAATCAAGT ATGAATGGTC CTCAAAAACC TGAAGATAGA
1021 GCGGGGCGTG GTGGCATAACA CTTTATTCC CAGCACTGGG GAGGCAGAGG CAGGTGGATC
1081 TCTGAGTTCC AGGCCAGCCT GGTCTATAGC ACAGGTCTA GGACAGCCAG GGCTACACAG
1141 AAAAAACCTG CCTTGATTAA ACCAAACCAA ACCAAACCAA ACCAAACCAA ACCAAACCAA
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Figure 5 (continued):

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1921 GTTTTTACAG AGCCCTGGTC TATGCCTTTA TCCTCCTCTG GCAGCTTCGG AGTTTCATTT
1981 CTTACATTTA GATCTTTGAT CCACCTTGAA CAAGTTTGG AGCAGGGTGA GAGATACGAA
2041 TCTAGTTCCA TTCTTCCATA TGTGATCCTA GTTTACATAG CATCGTTGGT TGAAGAGGTT
2101 TTATTTTATT TTTAAATAAT GTGTCATAAA AAACGAGGTG GTTGTAGCAG TGTGGATTG
2161 TTTCTTTGTC CTTTGATCTA CAGGTCTTGT TTTGTGTGAG TCTCATGATG TTTTATTGCT
2221 ATGGCTCTGT CATAAGTCTT GAGGTGAGGT ATTGTGATAT ACCTTCAGTA TTGCTCCCTC
2281 AGACTCAGGT TTGCTTTGGC CAGGAGTCAT CTTACTCAGT GCTCTTAGAG CTCCCCCAGC
2341 ATGTAGCTGC TACTATTCTT AGTTGATAAA TCAGGAAACT GGGGCTCAGA GAGATTAAGT
2401 GTCTTGAAC ACTTCTGGGG AGGTGAAACG TGGAGACACT AAAGTGTGTT TACCCTGTAC
2461 TGTCTCGGT GCTGTGCGGT GCTGGGCTAC AGCAAAGCAC CTATACTATA TATTCTCAG
2521 GAGGTGGAAA AACTCAGCCT CCCTTGGGGT TCCCAAGCTC CCAGGTGTCC AGTCACTGCT
2581 GGAAACCTCA TGGAGTCTGA AAGGAAGGGT TGAGGGTACA TGGGGCAGCG ATGAGGAGCC
2641 TGGGGCTGGG ATCTCCCAA CACCTGGATA TCCAGATGCC ACTGGGTGAG GGGGAGTTGG
2701 GAACAGAGTT GGGATGTCCA TGGACCTGTG ACAAGGCCAG GGCCAGGGGG AGGATAACTC
2761 TGGCTTTACT AATTGCGAA AGTCTTAGC TTAGCAGCAG TTGTCTGGGA GCACAGAGGG
2821 GCCTTCTGTA AGAGGCTCAG GCAGTCCGCG TCTGTAGGCG AAGGTCTTCT CCATGTTCCC
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2941 TTGTGGAAAA TGGGTGCACA CCACCTTCTC AGGGTGGACC AGAGATCAAA TACCTTTTGC
3001 AGGGAGGAAT ATCTGGGAAG GGACGCTTAC TGGCTAAACC CTCAGGGCCT CTAGATACAT
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5461 ATAAAGCTTA AGGCATGACT ACATTAATAAT GCCTTTGCAA AGTATATGTG CCCTCTTCCA
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Figure 5 (continued):

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9001 GCCCTAATGA AGATGGGGCA GAAGACTGAA GGAATGGCCA ACCAATAACT GGCCCAACTT
9061 GAGACCCATC CTACAGGCAA GCATCAATTC CTGACACTAC TAATGATACT CTGTTATGCT
9121 TGCAGACAGA AGCCTAGCAT AACTATCCTC CGAGAGGTCC ACCCAGCAAC TGACTGAAAC
9181 AGAAAAAGAT ATCCACAGGC AAACAGTGGA TGGAGTCTAG GGACTATTAT GGGAGAGCTG
9241 TGGGAAGGAT TAAAAACCTT GAAGGGGATA GGAACCCAC AGGAAGACCA ACAGAGTCAA
9301 CTAAGAGACC TGTGGGAGCT CTCAGAGACT GAGCCACCAA CCAAAGAGCA TACACAGGCC
9361 GGTCCGAGGC ACCTGCGACG TGTGAAGCAG ACATGCAGCT CAGTCTCCAT GTAGGTCCCTC
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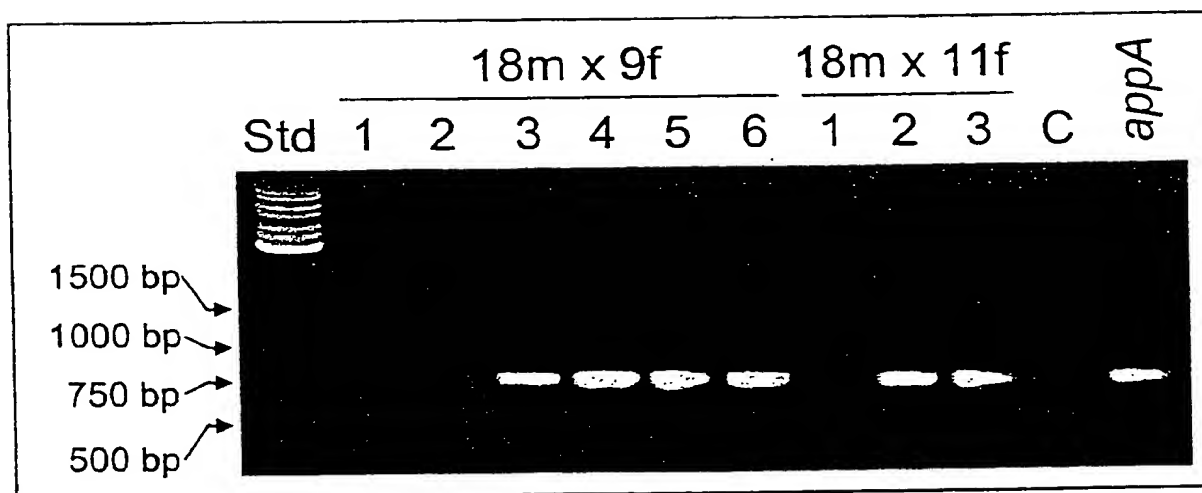
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9661	GCTCTGTCTT	GTTCCCTCAGC	CCAAGGCTCA	GCTCCACCT	GTTTCTGTGT	TTTTCTGGCT
9721	TTTCATGGGC	CTAGGACTTG	GTGACCAGT	CAACAATAGG	GGCCTGTGGA	AGACACAATA
9781	TACAAGACTA	GGGACATTCC	TGTTCTGTGT	ACTATCCATA	GCCTGATGTA	GGGTGGAAGGA
9841	CCCAATCAGT	GGAATTTCTAC	CTTTGCACAA	CCTTGACAGC	TGAGGGCCTC	TCAGAAACCT
9901	ATTTCTTCCA	CTGAAAAATG	AGACTCTCAA	ATGAACGTCG	TGACAATCAT	CAGGCTTATT
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10021	TAGGAAGGAC	AAGAACTGCT	CACCTGCTGC	CCCCAGGAGG	CCATTTGCTG	AAACAGCTGC
10081	TCTCCTGTCT	GTGCACAGGC	CTCGCCTTCT	CATTGCAAGC	ACAGGCCCTT	CTGTCTGTAA
10141	CCTCCTGTCA	GGTCACTGGG	AAAACAGATCA	AGATGGAACA	GGACAGCTCC	TGATGGTAAA
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10261	GAGCTGTGGG	CATGAACCAC	AGTGTTCGAG	GTAGAGTTGG	GGTTCTGAAA	TTACAGCTGG
10321	GGTGAGCTCA	GTAATGTGTA	GCTGGAGGTC	ACTCGTGAGA	CACACAGTCC	TGCTGCTTCT
10381	GTTCCCAAGT	TCCTGAGGAG	ACGACAGATC	TACTTTGTGT	AGAGGCCACA	GTCTAGTTGA
10441	CCTGAGAGTT	ACCAGTTTCT	TATTTGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG
10501	TGTTGTTTCGT	GTGTGAGTGC	AGGTGCACAT	ATGATAGCGT	ACACGTTGAG	GTGAGAGGAT
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10621	TTATTCAGG	GGAGCAAGTC	GCTGTTGGCT	GACACATCTT	GCTCACATAC	ATTTTACCTA
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10741	CTCTACCCAC	ATAGGAGTTG	GGTCTCCACA	CACCCCCACA	CCCCCTTCA	CAAAACGTTT
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12241	AAAGTGAGCA	GGCAAGGCAG	GGAATGTGTT	GCATATGTAT	ATGTACATGA	ATATATTATG
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12361	TCTCTTAACT	GCTAAGCACA	ATGACTTCCA	GTTCCATCCA	TTTCTGAAA	TGCCCAACTT
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12541	TCTTGTTGAA	AGGCAAGCGT	GAGAGAGGCA	GGCACTAATT	GTGGGTTTTT	GTTTCTTCTT
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12661	CATCTTAATC	CCATTTTAT	CTCTTCTGAT	TCCGTTAACC	CCGCAATCTG	CATTGCTGTC
12721	GAGTGAGAGC	GAGCTGAAGC	TGGAAGTGTG	GGTGATTGTC	AGTCGTCTAG	GTGTGCGTGC
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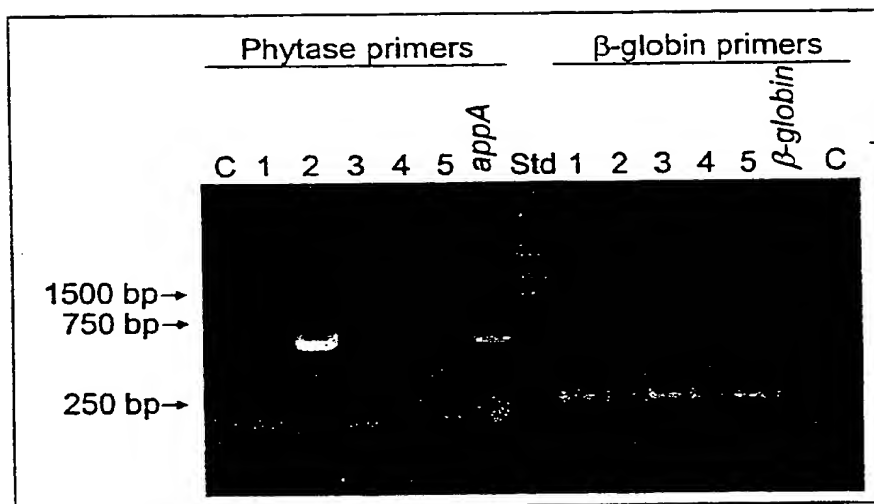
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13561	CCATCCACCG	CAAAAACAGG	CGTATGGTGT	GACATTACCC	ACTTCAGTGC	TGTTTATCGC
13621	CGGACACGAT	ACTAATCTGG	CAAATCTCGG	CGGCGCACTG	GAGCTCAACT	GGACGCTTCC
13681	CGGTGAGCCG	GATAACACGC	CGCCAGGTGG	TGAACTGGTG	TTTGAACGCT	GGCGTCGGCT
13741	AAGCGATAAC	AGCCAGTGGA	TTCAGGTTTC	GCTGGTCTTC	CAGACTTTAC	AGCAGTCCG
13801	TGATAAAACG	CCGCTGTCAT	TAAATACGCC	GCCCAGAGAG	GTGAAACTGA	CCCTGGCAGG
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14461	CCAGAAGGAA	CTTAGAGGAT	AGCTCATAAC	TTAAAAAGAA	ATGTAGAGAG	TAGCAGAAAC
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15241	AACTGTAGGC	CCAGTCCTTG	GTGTCCAAAA	TGGGTTTTAT	GGTTTGAATC	TGCAAAAGCCT
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16681	TGCTACCAAT	TTGACATTTG	TAGACCTGCT	ATTGTGTGCT	TCTTTATTGG	GCTCTCCCAT
16741	CTCCCAACTT	TCCAACCCAT	ATTCCACATT	AATCCCTTCC	ACCACCATGC	AACACTAGGT
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17221	CATAACTGTT	TTTTTTTTCC	AATTTTTTAT	TAGGTATTTT	CTTTATTTAC	ATTTCAAATG
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Figure 5 (continued):

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17461	CTCTGGGGGT	ACTAGTTAGT	TCATATTGTT	GTTCCACCTA	TAGGGTCGCA	GACCCCTTCA
17521	GCTCCTTGGG	TACTTTGTCT	AGCTCCTCCA	CTGGGGGCTC	TGTGTTTTAT	CTAATAGATG
17581	ACTGTGAGCA	TCCACTTCTG	TATTTGACAG	GCACTGGCCT	AGCGTCACAT	GAGCCAGCTA
17641	TATCAGGGTC	CTTTCAGCAA	AACCTTGCTG	GCATGTGCAA	TAGTGTCTGC	GTTTGGTGGT
17701	TGATTATGGG	ATGGATCCAC	TAGTTCTAGA	GCGGCCGCCA	CCGCGGTGGA	GCTCCAGCTT
17761	TTGTTCCCTT	TAGTGAGGGT	TAATTGCGCG	CTTGGCGTAA	TCATGGTCAT	AGCTGTTTCC
17821	TGTGTGAAAT	TGTTATCCGC	TCACAATTCC	ACACAACATA	CGAGCCGGAA	GCATAAAGTG
17881	TAAAGCCTGG	GGTGCCTAAT	GAGTGAGCTA	ACTCACATTA	ATTGCGTTGC	GCTCACTGCC
17941	CGCTTTCAG	TCGGGAAACC	TGTCGTGCCA	GCTGCATTAA	TGAATCGGCC	AACGCGCGGG
18001	GAGAGGCGGT	TTGCGTATTG	GGCGCTCTTC	CGCTTCTCG	CTCACTGACT	CGTGCCTC
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18121	AGAATCAGGG	GATAACGCAG	GAAAGAACAT	GTGAGCAAAA	GGCCAGCAAA	AGGCCAGGAA
18181	CCGTAAAAAG	GCCGCGTTGC	TGGCGTTTTT	CCATAGGCTC	CGCCCCCTG	ACGAGCATCA
18241	CAAAAATCGA	CGCTCAAGTC	AGAGGTGGCG	AAACCCGACA	GGACTATAAA	GATACCAGGC
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18361	CCTGTCCGCT	TTTCTCCCTT	CGGGAAGCGT	GGCGCTTTCT	CATAGCTCAC	GCTGTAGGTA
18421	TCTCAGTTCG	GTGTAGGTCG	TTGCTCCAA	GCTGGGCTGT	GTGCACGAAC	CCCCCGTTCA
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18601	TGCTACAGAG	TTCTTGAAGT	GGTGGCCTAA	CTACGGCTAC	ACTAGAAGGA	CAGTATTTGG
18661	TATCTGCGCT	CTGCTGAAGC	CAGTTACCTT	CGGAAAAAGA	GTTGGTAGCT	CTTGATCCGG
18721	CAAAACAAACC	ACCGCTGGTA	GCGGTGGTTT	TTTTGTTTGC	AAGCAGCAGA	TTACGCGCAG
18781	AAAAAAAGGA	TCTCAAGAAG	ATCCTTTGAT	CTTTTCTACG	GGGTCTGACG	CTCAGTGGAA
18841	CGAAAACCTCA	CGTTAAGGGA	TTTTTGGTCAT	GAGATTATCA	AAAAGGATCT	TCACCTAGAT
18901	CCTTTTAAAT	TAAAAATGAA	GTTTTAAATC	AATCTAAAGT	ATATATGAGT	AAACTTGGTC
18961	TGACAGTTAC	CAATGCTTAA	TCAGTGAGGC	ACCTATCTCA	GCGATCTGTC	TATTTGTTTC
19021	ATCCATAGTT	GCCTGACTCC	CCGTGCTGTA	GATAACTACG	ATACGGGAGG	GCTTACCATC
19081	TGGCCCCAGT	GCTGCAATGA	TACCGCGAGA	CCCACGCTCA	CCGGCTCCAG	ATTTATCAGC
19141	AATAAACCAG	CCAGCCGGAA	GGGCCGAGCG	CAGAAAGTGG	CCTGCAACTT	TATCCGCCTC
19201	CATCCAGTCT	ATTAATTGTT	GCCGGGAAGC	TAGAGTAAGT	AGTTCGCCAG	TTAATAGTTT
19261	GCGCAACGTT	GTTGCCATTG	CTACAGGCAT	CGTGGTGTC	CGCTCGTCGT	TTGGTATGGC
19321	TTCATTAGC	TCCGTTTCCC	AACGATCAAG	GCGAGTTACA	TGATCCCCCA	TGTTGTGCAA
19381	AAAAGCGGTT	AGCTCCTTCG	GTCCTCCGAT	CGTTGTCAGA	AGTAAGTTGG	CCGAGTGT
19441	ATCACTCATG	GTTATGGCAG	CACTGCATAA	TTCTCTTACT	GTCATGCCAT	CCGTAAGATG
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19561	GAGTTGCTCT	TGCCCGGCGT	CAATACGGGA	TAATACCGCG	CCACATAGCA	GAACCTTAAA
19621	AGTGCTCATC	ATTGGAAAAC	GTTCTTCGGG	GCGAAAACTC	TCAAGGATCT	TACCGCTGTT
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20041	GGCAAAATCC	CTTATAAATC	AAAAGAATAG	ACCGAGATAG	GGTTGAGTGT	TGTTCCAGTT
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20401	CTACAGGGCG	CGTCCCATT	GCCATTTCAG	CTGCGCAACT	GTTGGGAAGG	GCGATCGGGT
20461	CGGGCCTCTT	CGCTATTACG	CCAGCTGGCG	AAAGGGGGAT	GTGCTGCAAG	GCGATTAAGT
20521	TGGGTAAACG	CAGGGTTTTT	CCAGTACGCA	CGTTGTAAAA	CGACGGCCAG	TGAGCGCGCG
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**Figure 6**

**Figure 7**

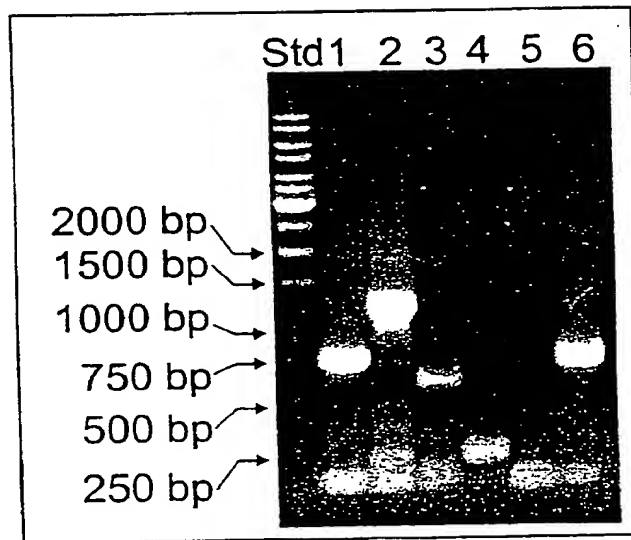


Figure 8

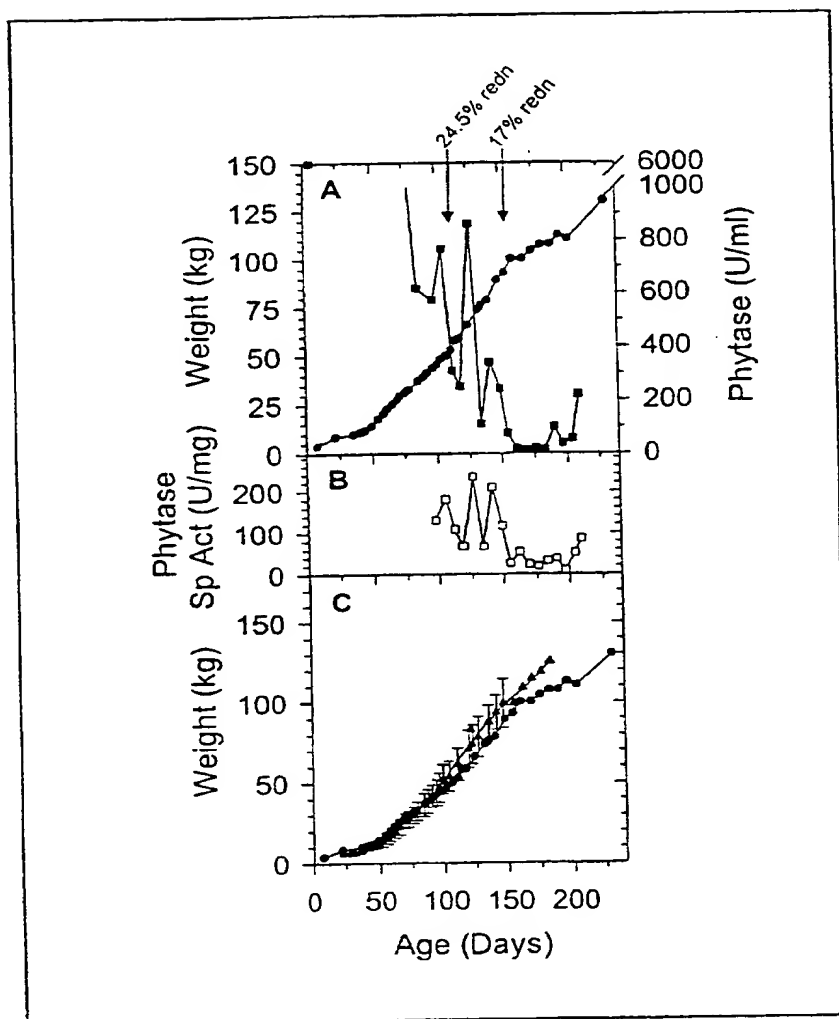


Figure 9

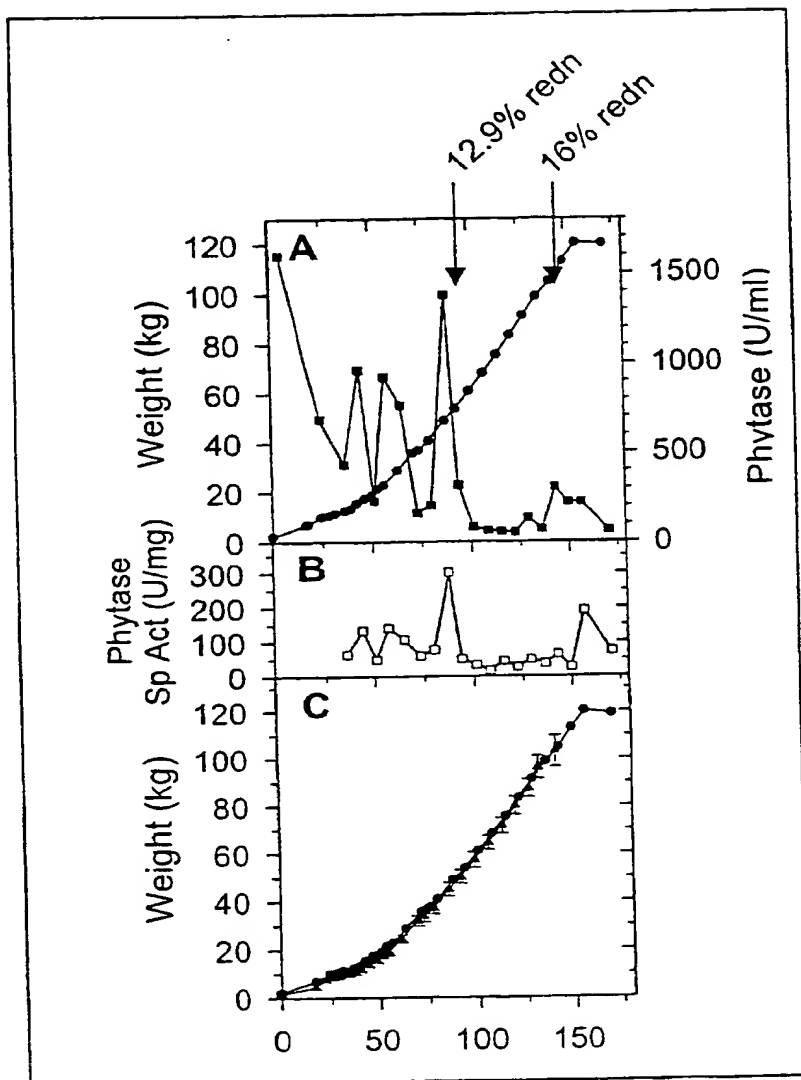


Figure 10

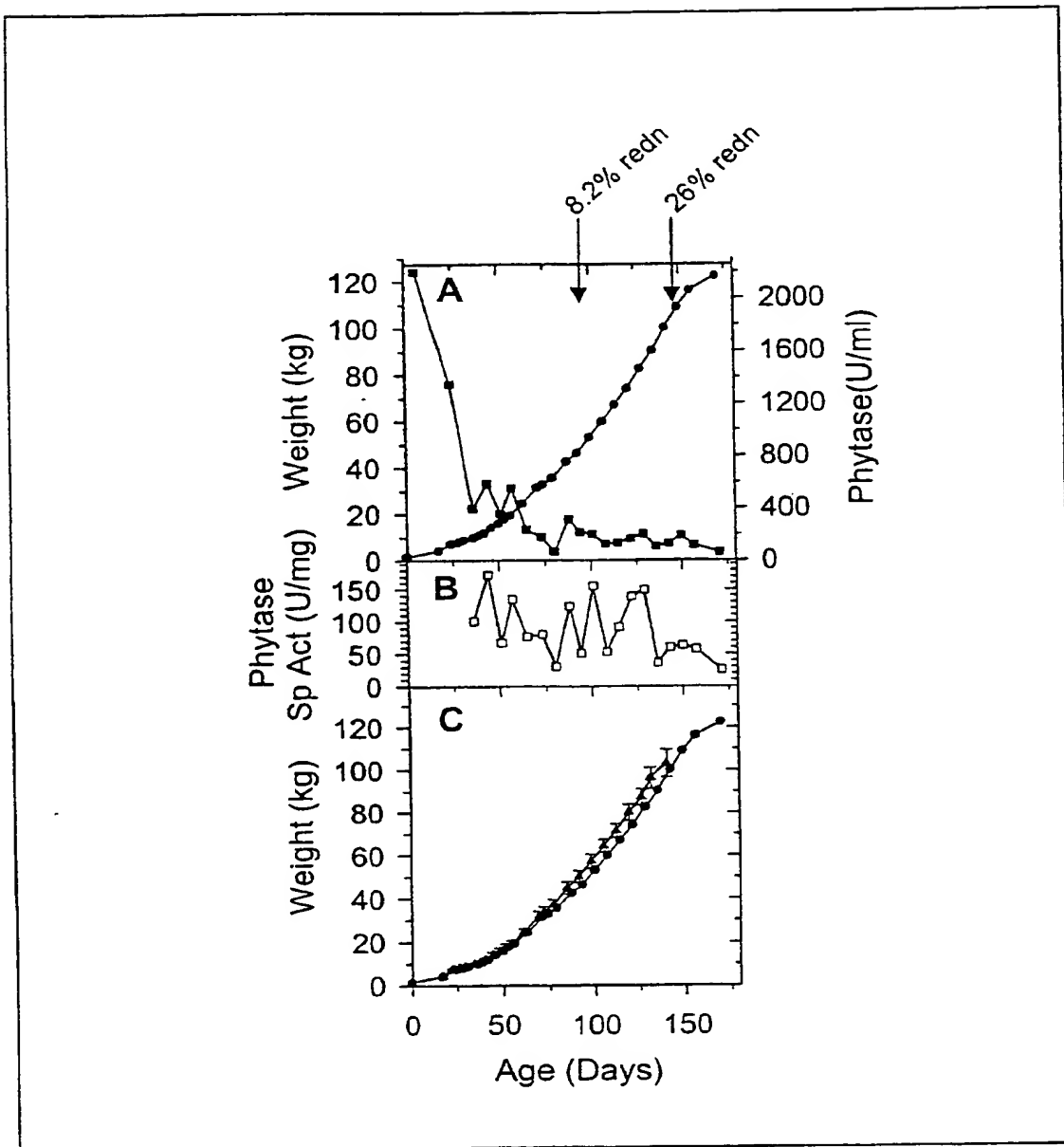
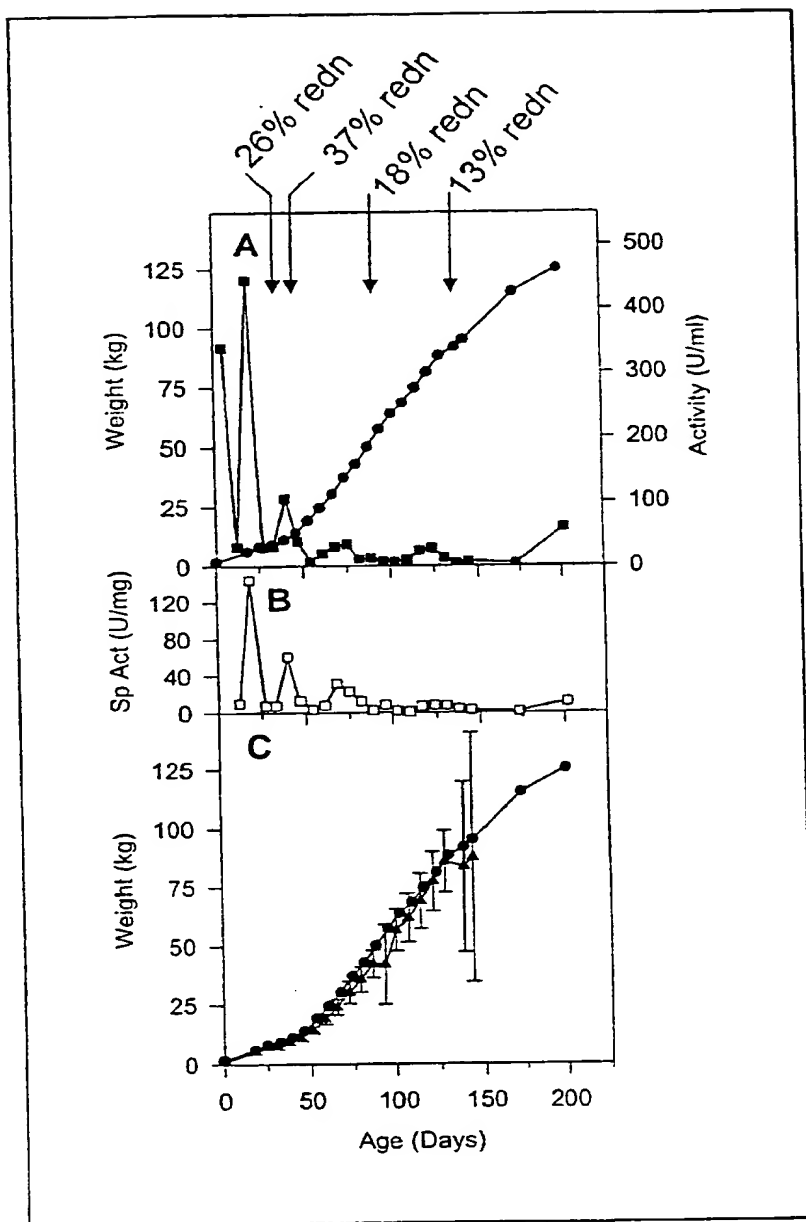


Figure 11

**Figure 12**

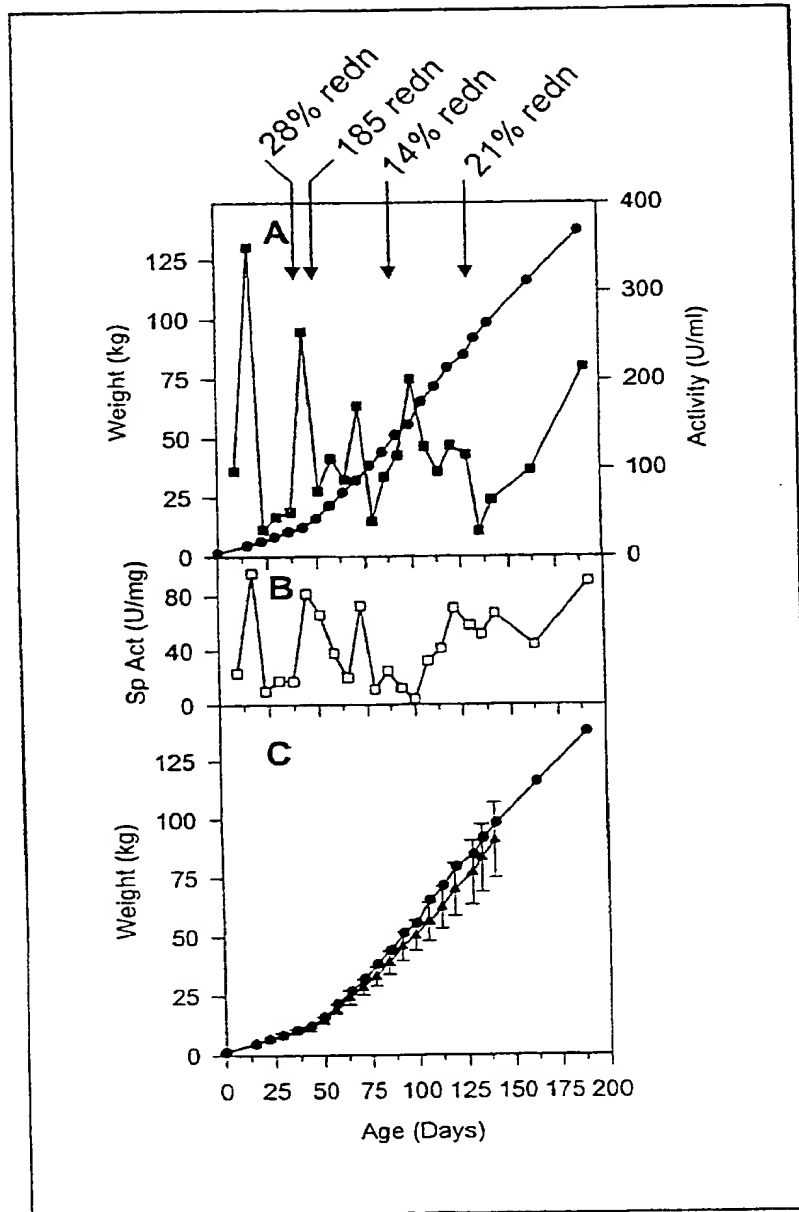


Figure 13

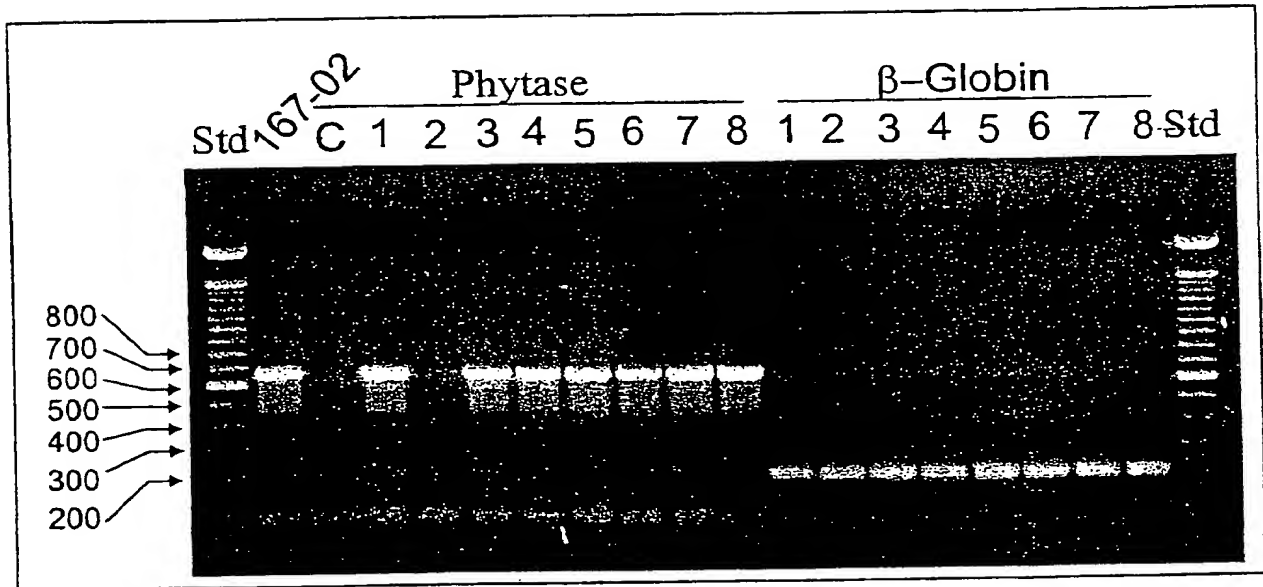


Figure 14

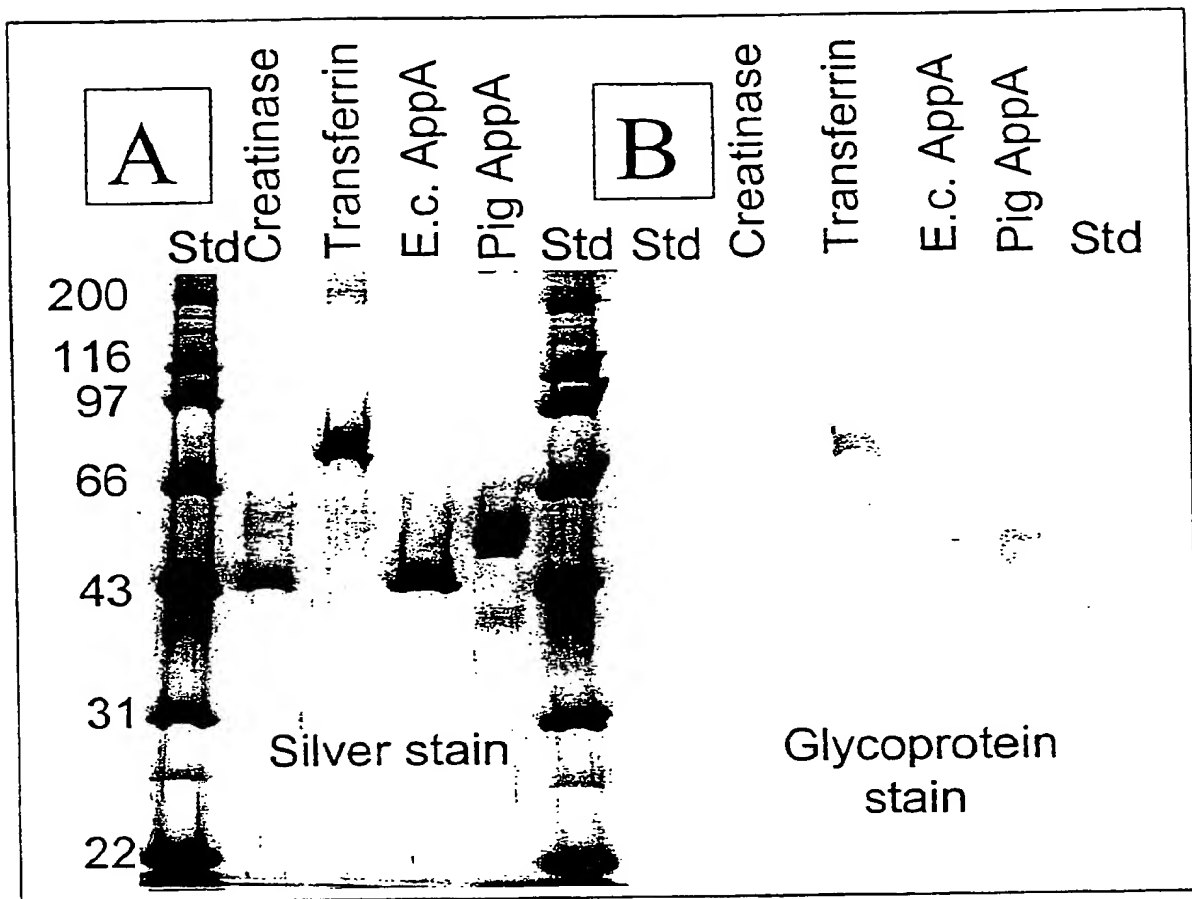


Figure 15

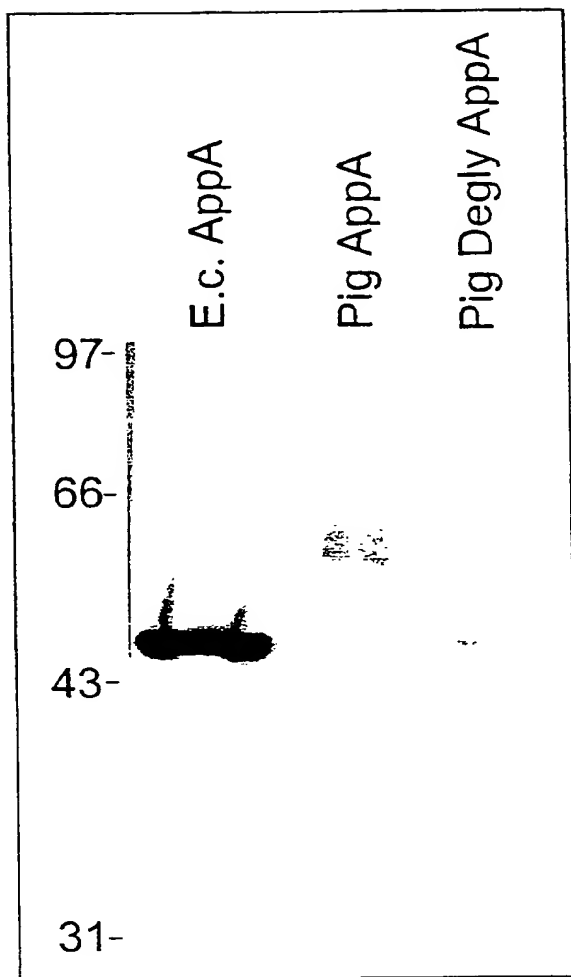


Figure 15B

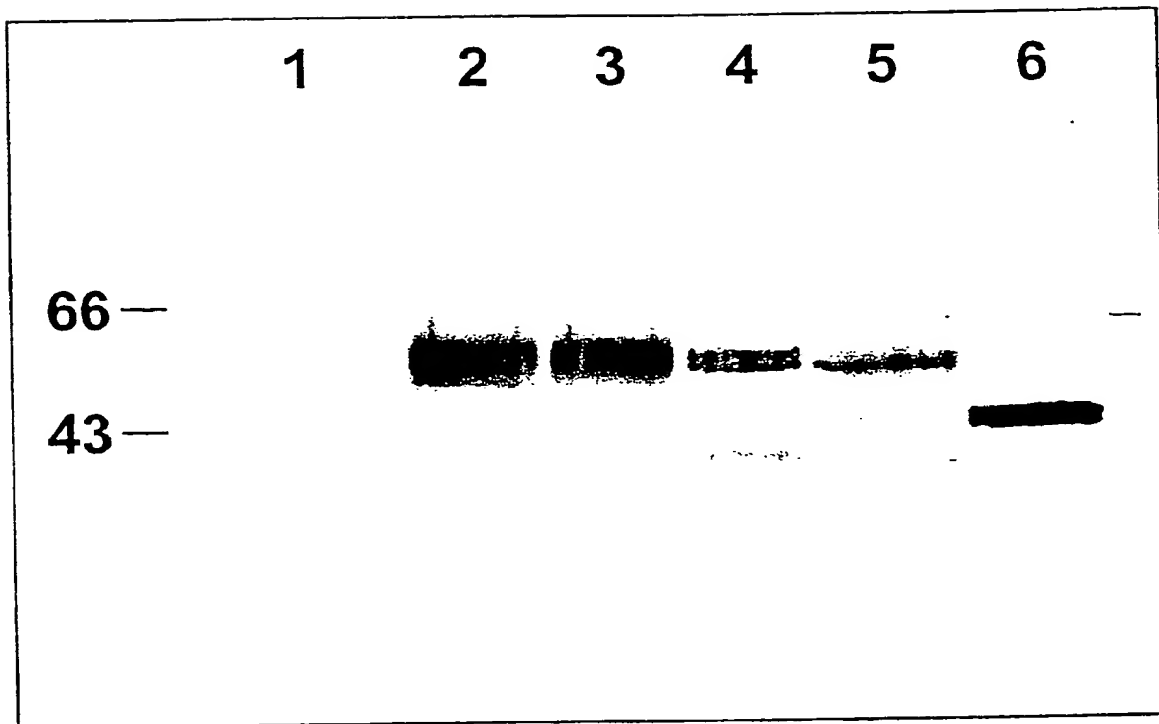


Figure 16

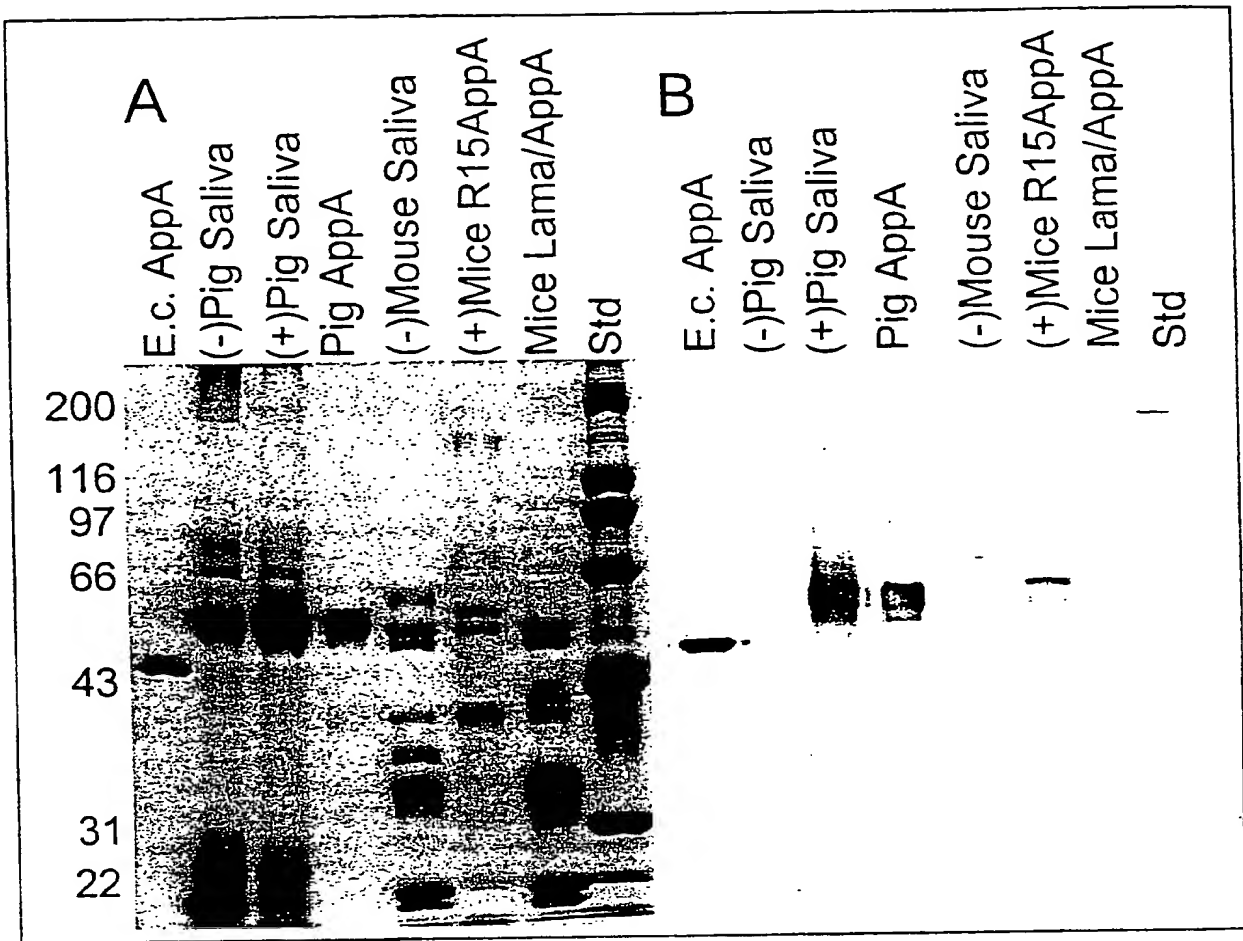


Figure 17

Figure 18: Nucleic acid sequence of the known segment of the R15/appa+intron plasmid, including the vector sequences of pBLCAT3 (SEQ ID NO:2).

LOCUS R15/appa+intron 6708 bp DNA SYN 15-APR-2000
 DEFINITION R15/appa+intron transgene with vector cut 13543 to 4954
 ACCESSION R15/appa+intron
 REFERENCE 1 (bases 1 to 6708))
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequence.
 KEYWORDS salivary proline-rich protein, acid glucose-1-phosphatase; appA
 gene; periplasmic phosphoanhydride phosphohydrolase; artificial
 sequence;
 AUTHORS Golovan, S., Forsberg, C.W., Phillips, J.
 JOURNAL Unpublished.

DEFINITION Rat salivary proline-rich protein (RP15) gene.
 ACCESSION M64793 M36414
 VERSION M64793.1 GI:206711
 SOURCE Rat (Sprague-Dawley) liver DNA.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 1748)
 AUTHORS Lin, H.H. and Ann, D.K.
 TITLE Molecular characterization of rat multigene family
 encoding
 proline-rich proteins
 JOURNAL Genomics 10, 102-113 (1991)
 MEDLINE 91257817
 FEATURES Location/Qualifiers
 source 1..1748
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /tissue_type="liver"
 /tissue_lib="cosmid genomic library"
 misc_feature 1802-1810
 /function=" consensus sequence for initiation in
 higher eukaryotes "

FEATURES Location/Qualifiers
 DEFINITION E. coli periplasmic phosphoanhydride phosphohydrolase (appA)
 gene,

ACCESSION M58708 L03370 L03371 L03372 L03373 L03374 L03375
 VERSION M58708.1 GI:145283
 SOURCE Escherichia coli DNA.
 ORGANISM Escherichia coli
 Bacteria; Proteobacteria; gamma subdivision;
 Enterobacteriaceae;
 Escherichia.
 REFERENCE 1 (bases 1811..3109)
 AUTHORS Dassa, J., Marck, C. and Boquet, P.L.

Figure 18 (continued):

TITLE The complete nucleotide sequence of the Escherichia coli gene appA reveals significant homology between pH 2.5 acid phosphatase and glucose-1-phosphatase

JOURNAL J. Bacteriol. 172 (9), 5497-5500 (1990)

MEDLINE 90368616

FEATURES Location/Qualifiers

Source 1811..3109
/organism="Escherichia coli"
/db_xref="taxon:562"

sig_peptide 1811.. 1876
/gene="appA"

CDS 1811..3109
/gene="appA"
/standard_name="acid phosphatase/phytase"
/transl_table=11
/product="periplasmic phosphoanhydride phosphohydrolase"
/protein_id="AAA72086.1"
/db_xref="GI:145285"

/translation="MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAP
TKATQLMQDVTTPDAWPTWPVKLGWLTTPRGELIAYLGHYQRQLVADGLLAKKGCPOS
GQVAIIADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNA
NVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPS
ELKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQF
YLLQRTPEVARSRATPLLDLIKALTTPHPPQKQAYGVTLPSTSVLFIAGHDTNLANLGG
ALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIVSLVFQTLQQMRDKTPLSLNT
PPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSL"

mat_peptide 1877 3106
/gene="appA"
/product="periplasmic phosphoanhydride phosphohydrolase"

mutation replace(1817.. 1819,"gcg changed to gcc")
/gene="appA"
/standard_name="A3 mutant"
/note="created by site directed mutagenesis"
/phenotype="silent mutation"

mutation replace(3092..3094," ccg changed to ccc")
/gene="appA"
/standard_name=" P428 mutant"
/note="created by site directed mutagenesis"
/phenotype=" silent mutation "

mutation replace(3095..3097," gcg changed to gct")
/gene="appA"
/standard_name=" A429 mutant"
/note="created by site directed mutagenesis"
/phenotype=" silent mutation "

Figure 18 (continued):

DEFINITION Plasmid pBLCAT3 (bases 3109 to 6708)

ACCESSION X64409
 VERSION X64409.1 GI:58163
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequence.
 REFERENCE 1 (bases 3109 to 6708)
 AUTHORS Luckow,B.H.R.
 TITLE Direct Submission
 JOURNAL Submitted (06-FEB-1992) B.H.R. Luckow, German Cancer Res
 Center, Im Neuenheimer Feld 280, W-6900 Heidelberg, FRG
 REFERENCE 2 (bases 3109 to 6708)
 AUTHORS Luckow,B. and Schutz,G.
 TITLE CAT constructions with multiple unique restriction sites

for

the functional analysis of eukaryotic promoters and
 regulatory elements

JOURNAL Nucleic Acids Res. 15 (13), 5490 (1987)
 MEDLINE 87260024
 COMMENT Promoterless CAT vector for transient transfection
 experiments

with eukaryotic cells. Allows the analysis of foreign
 promoters and enhancers.

FEATURES Location/Qualifiers
 source 3109 to 6116
 /organism="synthetic construct"
 /db_xref="taxon:32630"

SV40 t intron 3197..3810
 /note="SV40 signals"
 polyA_signal 3807..4047
 /note="SV40 signals"
 CDS complement(5244..6104)
 /codon_start=1
 /transl_table=11
 /gene="Amp"
 /product="beta-lactamase"
 /protein_id="CAA45753.1"
 /db_xref="GI:58165"

BASE COUNT 1916 a 1479 c 1515 g 1798 t
 ORIGIN

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61 GAGAGTCCTG TTTGGTTTAA GCAACCTCTG TTTCTCATAA ACTCCATAAA AACAGGAATA
121 CTCTTTGTTT CTAGCATAAC CAAAAGATTT AGTGAATTGA AAACAATGTT CCCTTAGAGT
181 ATAGGTCTAA TAACCCCGAA AATATTACCA TGATACTGAG CATTTGTAAG TATCTCATAG
241 CATGTAGTAT CCATAGTCCA TCAATGAGAG AGACATTTAA CATGATTTTC ATTAATCAGG
301 TGGAAAAGAC ATGACAACAT TCACAGGCAC TGCACAGAAC ATAGTGGTCC ACCTTGCACA
361 TATTTCACTA AACTAGGTTT ATCTATTTTG TTGCTTTCTC TAACATCTCT GCAATGAAGC
421 AGGTCAACAG TGCCACATAT CCTTTACTTA ACCTAAGGAA CACAAAAAAT TTTCTACATA
481 TATCCTGGTT AGAGAGTGCT TAAAATAAGT TTTCCAAGAA TGGAAAAGAA ATGTTCTGAC
541 TTAACAATTA AGACAGTATT TATTTAAAGC AAGAAATATG AGGCACACAA GAAAATATTT
601 TGGGAAGAAA CCATTTGGTG AACAAATATT CAAATAAAAA TAGACAAACA TAGTTAATTG
661 TAAAAACATAT GTTTGACCAG CCCTTCTTTT CAATAGGCTT AATGTGAATA AAATGTTAAA
721 GATTCTCTTT GGGTGGCTGC AAATTGTCCA CGAATAAGAC AAAATATAAA AATAAGGACT
781 GAGTCTCACA AAATGAAAAG GAAATATATT CAGAAAGAGA ATCTTGAGAG AATGTGTTGT
841 CACAAATTAA AGAAAACCTG TGGTGAATGA CATCCTGAGG CCTGAGCTAT TACTGACATT

```

Figure 18 (continued):

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901 TAAGATAAAG GTAACGTGTAT ACATTTGTCC CATTGAGGGG ACAAGAAAGC TGCTCTCATG
961 TTCAGCTCTA TAATTCTTGC CTTAAACAAC TTAAATAGAA TGATTTAAAA TATGGAGCTG
1021 TCCATGGACC TTTGAAATAT AAAATAGTCA AGCAACTTAT CAAGGAATTA CAGATTCCTT
1081 GATACTAACA CAGGTAAATC CCACACGTGT TTTGAGACTA CATTTGCTGG GATTTTATTG
1141 ATGTAATAGG TCACATGTTT TTCGGGCCAA TGTTGCTGTT ATTCGGTTAC TTCAAGAGAA
1201 TAGTGGCAAC TGATGCTATG TATTCTAGGG GTTTGAAGTG ATGTTTCATG ATTGAAATTT
1261 GTAAAAGAAT AACATCATCA TTCTTAACAA TAGAACATAT AAAGTCACAC AGAAGTGACA
1321 GTGTTTAAGC TGTACTATTG ATCAAAGAAA TTTATTACCT TCAGTTTCAA TGGAAATAAT
1381 TACTGATAAT ACAAACATGT GTGAACACAC ACTAATCCTA TCCAAATGCA CAGTGATACA
1441 CAGAAAATAT TAGCAAGTAG AATGCAATAT TTATATAACG ATTGTATTTA TCAATCAATT
1501 GTATGTATCA ATATATGGGC TATTTTCTTA CACATGATTT TATTCAAAT TACTCTAATC
1561 ATTGTTGAAC CATTTAGAAA AGGCATACTG GCAACTTTTC CTTACCTCAT CCAGCTGGGC
1621 AAAAGTCCCA GTGTGGAGTA AAGGATGCAA GATTTCTGCT TCTGTTAAGT ATAAAATAAT
1681 AGTATGAATT CAAAGGTGCC ATTCTTCTGC TTCTAGTTAT AAAGGCAGTG CTTGCTTCTT
1741 CCAGCACAGA TCTGGATCTC GAGGAGCTTG GCGAGATTTT CAGGAGCTAA GGAAGCTAAA
1801 AGCCGCCACC ATGAAAGCCA TCTTAATCCC ATTTTATCT CTTCTGATT CGTAAACCCC
1861 GCAATCTGCA TTCGCTCAGA GTGAGCCGGA GCTGAAGCTG GAAAGTGTGG TGATTGTCAG
1921 TCGTCATGGT GTGCGTGCTC CAACCAAGGC CACGCAACTG ATGCAGGATG TCACCCAGA
1981 CGCATGGCCA ACCTGGCCGG TAAACTGGG TTGGCTGACA CCGCGCGGTG GTGAGCTAAT
2041 CGCCTATCTC GGACATTACC AACGCCAGCG TCTGGTAGCC GACGGATTGC TGGCGAAAAA
2101 GGGCTGCCCG CAGTCTGGTC AGGTCGCGAT TATTGCTGAT GTCGACGAGC GTACCCGTAA
2161 AACAGGCGAA GCCTTCGCCG CCGGGCTGGC ACCTGACTGT GCAATAACCG TACATACCCA
2221 GGCAGATACG TCCAGTCCCG ATCCGTTATT TAATCCTCTA AAAACTGGCG TTTGCCAACT
2281 GGATAACGCG AACGTGACTG ACGCGATCCT CAGCAGGGCA GGAGGGTCAA TTGCTGACTT
2341 TACCGGGCAT CGGCAAACGG CGTTTCGCGA ACTGGAACGG GTGCTTAATT TTCCGCAATC
2401 AAACCTTGTC CTTAAACGTG AGAAACAGGA CGAAAGCTGT TCATTAACGC AGGCATTACC
2461 ATCGGAACCT AAGGTGAGCG CCGACAATGT CTCATTAACC GGTGCGGTAA GCCTCGCATC
2521 AATGCTGACG GAGATATTTC TCCTGCAACA AGCACAGGGA ATGCCGAGC CGGGGTGGGG
2581 AAGGATCACC GATTACACAC AGTGGAACAC CTTGCTAAGT TTGCATAACG CGCAATTTTA
2641 TTTGCTACAA CGCACGCCAG AGGTTGCCCG CAGCCGCGCC ACCCGTTAT TAGATTTGAT
2701 CAAGACAGCG TTGACGCCCC ATCCACCGCA AAAACAGGCG TATGGTGTGA CATTACCCAC
2761 TTCAGTGCTG TTTATCGCCG GACACGATAC TAATCTGGCA AATCTCGGCG GCGCACTGGA
2821 GCTCAACTGG ACGCTTCCCG GTCAGCCGGA TAACACGCCG CCAGGTGGTG AACTGGTGT
2881 TGAACGCTGG CGTCGGCTAA GCGATAACAG CCAGTGATT CAGGTTTCGC TGTCTTCCA
2941 GACTTTACAG CAGATGCGTG ATAAAACGCG GCTGTCATTA AATACGCCG CCGGAGAGGT
3001 GAAACTGACC CTGGCAGGAT GTGAAGAGCG AAATGCGCAG GGCATGTGTT CGTTGGCAGG
3061 TTTTACGCAA ATCGTGAATG AAGCAGCAT ACCCGCTTGC AGTTTGTAAG GTATAAGGCA
3121 GTTATTGGTG CCCTTAAACG CCTGGTGCTA CGCCTGAATA AGTGATAATA AGCGGATGAA
3181 TGGCAGAAAT TCGCCGGATC TTTGTGAAGG AACCTTACTT CTGTGGTGTG ACATAATTGG
3241 ACAAACCTACC TACAGAGATT TAAAGCTCTA AGGTAAATAT AAAATTTTAA AGTGATATAAT
3301 GTGTAAACT ACTGATTCTA ATTGTTGTG TATTTTAGAT TCCAACCTAT GGAAGTATG
3361 AATGGGAGCA GTGGTGGAAT GCCTTTAATG AGGAAAACCT GTTTTGCTCA GAAGAAATGC
3421 CATCTAGTGA TGATGAGGCT ACTGCTGACT CTCACATTG TACTCCTCCA AAAAAGAAGA
3481 GAAAGGTAGA AGACCCCAAG GACTTTCCTT CAGAAATGCT AAGTTTTTGT AGTCATGCTG
3541 TGTTTAGTAA TAGAACTCTT GCTTGCTTTG CTATTTACAC CACAAAGGAA AAAGCTGCAC
3601 TGCTATACAA GAAAATTATG GAAAAATATT CTGTAACCTT TATAAGTAGG CATAACAGTT
3661 ATAATCATAA CATACTGTTT TTTCTTACTC CACACAGGCA TAGAGTGTCT GCTATTAATA
3721 ACTATGCTCA AAAATTGTGT ACCTTTAGCT TTTTAATTTG TAAAGGGGTT AATAAGGAAT
3781 ATTTGATGTA TAGTGCCTTG ACTAGAGATC ATAATCAGCC ATACCACATT TGTAGAGGTT
3841 TTAAGTGTG TAAAAACCT CCCACACCTC CCCCTGAACC TGAAACATAA AATGAATGCA
3901 ATTGTTGTTG TTAAGTGTG TATTGCAGCT TATAATGGTT ACAAATAAAG CAATAGCATC
3961 ACAAATTTCA CAAATAAAGC ATTTTTCCTA CTGCATTCTA GTTGTGGTTT GTCCAAACTC
4021 ATCAATGTAT CTTATCATGT CTGGATCGAT CCCCAGGTAC CGAGCTCGAA TTCGTAATCA
4081 TGGTCATAGC TGTTTCCTGT GTGAAATTGT TATCCGCTCA CAATTCCACA CAACATACGA
4141 GCCGGAAGCA TAAAGTGTA AGCCTGGGT GCTTAATGAG TGAGCTAAGT CACATTAATT
4201 GCGTTGCGCT CACTGCCCGC TTTCCAGTCG GGAAACCTGT CGTGCCAGCT GCATTAATGA
4261 ATCGGCCAAC GCGCGGGGAG AGGCGGTTTG CGTATTGGGC GCTCTTCCGC TTCCTCGCTC
4321 ACTGACTCGC TGCGCTCGGT CGTTCGGCTG CGGCGAGCGG TATCAGCTCA CTCAAAGGCG

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Figure 18 (continued):

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4381 GTAATACGGT TATCCACAGA ATCAGGGGAT AACGCAGGAA AGAACATGTG AGCAAAAGGC
4441 CAGCAAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG CGTTTTTCCA TAGGCTCCGC
4501 CCCCCTGACG AGCATCACAA AAATCGACGC TCAAGTCAGA GGTGGCGAAA CCCGACAGGA
4561 CTATAAAGAT ACCAGGCGTT TCCCCCTGGA AGCTCCCTCG TCGCTCTCC GTTCCGACC
4621 CTGCCGCTTA CCGGATACCT GTCCGCTTTT CTCCCTTCGG GAAGCGTGGC GCTTCTCAA
4681 TGCTCACGCT GTAGGTATCT CAGTTCGGTG TAGGTCGTTT GCTCCAAGCT GGGCTGTGTG
4741 CACGAACCCC CCGTTCAGCC CGACCGCTGC GCCTTATCCG GTAACATCG TCTTGAGTCC
4801 AACCCGGTAA GACACGACTT ATCGCCACTG GCAGCAGCCA CTGGTAACAG GATTAGCAGA
4861 GCGAGGTATG TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGGCTACACT
4921 AGAAGGACAG TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG AAAAAGAGTT
4981 GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT TGTGTGCAAG
5041 CAGCAGATTA CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCTT TTCTACGGGG
5101 TCTGACGCTC AGTGGAACGA AAATCAGCT TAAGGGATTT TGGTCATGAG ATTATCAAAA
5161 AGGATCTTCA CCTAGATCCT TTAAATTA AAATGAAGTT TAAATCAAT CTAAAGTATA
5221 TATGAGTAAA CTTGGTCTGA CAGTTACCAA TGCTTAATCA GTGAGGCACC TATCTCAGCG
5281 ATCTGTCTAT TTCGTTTCAT CATAGTTGCC TGACTCCCCG TCGTGTAGAT AACTACGATA
5341 CGGGAGGGCT TACCATCTGG CCCCAGTGCT GCAATGATAC CGCGAGACCC ACGCTCACCG
5401 GCTCCAGATT TATCAGCAAT AAACCAGCCA GCCGGAAGGG CCGAGCGCAG AAGTGGTCCT
5461 GCAACTTTAT CCGCCTCCAT CCAGTCTATT AATTGTTGCC GGGAAGCTAG AGTAAGTAGT
5521 TCGCCAGTTA ATAGTTTGCG CAACGTTGTT GCCATTGCTA CAGGCATCGT GGTGTCACGC
5581 TCGTCGTTTG GTATGGCTTC ATTCAGCTCC GGTTCCTAAC GATCAAGGCG AGTTACATGA
5641 TCCCCCATGT TGTGCAAAAA AGCGGTTAGC TCCTTCGGTC CTCCGATCGT TGTGAGAAGT
5701 AAGTTGGCCG CAGTGTATAT ACTCATGGTT ATGGCAGCAC TGCATAATTC TCTTACTGTC
5761 ATGCCATCCG TAAGATGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCTGAGAA
5821 TAGTGATATG GCGGACCGAG TTGCTCTTGC CCGGCGTCAA TACGGGATAA TACCGCGCCA
5881 CATAGCAGAA CTTTAAAAGT GCTCATCATT GGAAAACGTT CTTGCGGGCG AAAACTCTCA
5941 AGGATCTTAC CGCTGTTGAG ATCCAGTTCG ATGTAACCCA CTCGTGCACC CAACTGATCT
6001 TCAGCATCTT TTACTTTCAC CAGCGTTTCT GGGTGAGCAA AAACAGGAAG GCAAAATGCC
6061 GCAAAAAAGG GAATAAGGGC GACACGGA AAATGAATAC TCATACTCTT CCTTTTCAA
6121 TATTATTGAA GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT TGAATGTATT
6181 TAGAAAAATA AACAAATAGG GGTTCGCGC ACATTTCCCC GAAAAGTGCC ACCTGACGTC
6241 TAAGAAACCA TTATTATCAT GACATTAACC TATAAAAAATA GGCGTATCAC GAGGCCCTTT
6301 CGTCTCGCGC GTTTCGGTGA TGACGGTGAA AACCTCTGAC ACATGCAGCT CCCGGAGACG
6361 GTCACAGCTT GTCTGTAAGC GGATGCCGGG AGCAGACAAG CCCGTCAGGG CCGCTCAGCG
6421 GGTGTTGGCG GGTGTCGGGG CTGGCTTAAC TATGCGGCAT CAGAGCAGAT TGTACTGAGA
6481 GTGCACCATA TCGGTGTGA AATACCGCAC AGATGCGTAA GGAGAAAAATA CCGCATCAGG
6541 CGCCATTGCG CATTACGGCT CGCAACTGT TGGGAAGGGC GATCGGTGCG GGCCTCTTCG
6601 CTATTACGCC AGCTGGCGAA AGGGGGATGT GCTGCAAGGC GATTAAGTTG GGTAACGCCA
6661 GGGTTTTCCC AGTCACGACG TTGTAAAACG ACGGCCAGTG CCAAGCTT

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Figure 19: Nucleic acid sequence of the known segment of the R15/appa-intron transgene used for the generation of transgenic mice (SEQ ID NO: 3).

LOCUS R15/appa 4060 bp DNA SYN 15-APR-2000
 DEFINITION R15/appa transgene without vector
 ACCESSION R15/appa
 REFERENCE 1 (bases 1 to 4060)
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequence.
 KEYWORDS salivary proline-rich protein, acid glucose-1-phosphatase; appA
 gene; periplasmic phosphoanhydride phosphohydrolase; artificial
 sequence;
 AUTHORS Golovan, S., Forsberg, C.W., Phillips, J.
 JOURNAL Unpublished.

DEFINITION Rat salivary proline-rich protein (RP15) gene.
 ACCESSION M64793 M36414
 VERSION M64793.1 GI:206711
 SOURCE Rat (Sprague-Dawley) liver DNA.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 1748)
 AUTHORS Lin, H.H. and Ann, D.K.
 TITLE Molecular characterization of rat multigene family
 encoding
 proline-rich proteins
 JOURNAL Genomics 10, 102-113 (1991)
 MEDLINE 91257817
 FEATURES
 source Location/Qualifiers
 1..1748
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /tissue_type="liver"
 /tissue_lib="cosmid genomic library"
 misc_feature 1802-1810
 /function=" consensus sequence for initiation in
 higher eukaryotes "

FEATURES Location/Qualifiers
 DEFINITION E. coli periplasmic phosphoanhydride phosphohydrolase (appA)
 gene,
 ACCESSION M58708 L03370 L03371 L03372 L03373 L03374 L03375
 VERSION M58708.1 GI:145283
 SOURCE Escherichia coli DNA.
 ORGANISM Escherichia coli
 Bacteria; Proteobacteria; gamma subdivision;
 Enterobacteriaceae;
 Escherichia.
 REFERENCE 1 (bases 1811..3109)
 AUTHORS Dassa, J., Marck, C. and Boquet, P.L.

Figure 19 (continued):

TITLE The complete nucleotide sequence of the Escherichia coli gene appA reveals significant homology between pH 2.5 acid phosphatase and glucose-1-phosphatase

JOURNAL J. Bacteriol. 172 (9), 5497-5500 (1990)

MEDLINE 90368616

FEATURES Location/Qualifiers

Source 1811..3109

/organism="Escherichia coli"

/db_xref="taxon:562"

sig_peptide 1811..1876

/gene="appA"

CDS 1811..3109

/gene="appA"

/standard_name="acid phosphatase/phytase"

/transl_table=11

/product="periplasmic phosphoanhydride phosphohydrolase"

/protein_id="AAA72086.1"

/db_xref="GI:145285"

/translation="MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAP

TKATQLMQDVTTPDAWPTWPVKLGWLTTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQS

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NVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPS

ELKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQF

YLLQRTPEVARSRATPLLDLIKALTTPHPPQKQAYGVTLPSTSVLFIAGHDTNLANLGG

ALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIVSLVFQTLQQMRDKTPLSLNT

PPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSL"

mat_peptide 1877 3106

/gene="appA"

/product="periplasmic phosphoanhydride phosphohydrolase"

mutation replace(1817..1819,"gcg changed to gcc")

/gene="appA"

/standard_name="A3 mutant"

/note="created by site directed mutagenesis"

/phenotype="silent mutation"

mutation replace(3092..3094,"ccg changed to ccc")

/gene="appA"

/standard_name="P428 mutant"

/note="created by site directed mutagenesis"

/phenotype="silent mutation"

mutation replace(3095..3097,"gcg changed to gct")

/gene="appA"

/standard_name="A429 mutant"

/note="created by site directed mutagenesis"

/phenotype="silent mutation"

Figure 19 (continued):

SV40 t intron 3197..3810
/note="SV40 signals"
polyA_signal 3807..4047
/note="SV40 signals"

BASE COUNT 1257 a 814 c 843 g 1146 t
ORIGIN

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61 GAGAGTCCTG TTTGGTTTAA GCAACCCTCTG TTTCTCATAA ACTCCATAAA AACAGGAATA
121 CTCTTTGTTT CTAGCATAAC CAAAAGATTT AGTGAATTGA AAACAATGTT CCCTTAGAGT
181 ATAGGTCTAA TAACCCCGAA AATATTACCA TGATACTGAG CATTTGTAAG TATCTCATAG
241 CATGTAGTAT CCATAGTCCA TCAATGAGAG AGACATTTAA CATGATTTTC ATTAATCAGG
301 TGGAAAAGAC ATGACAACAT TCACAGGCAC TGCACAGAAC ATAGTGGTCC ACCTTGACAC
361 TATTTCACTA AACTAGGTTT ATCTATTTTG TTGCTTTCTC TAACATCTCT GCAATGAAGC
421 AGGTCAACAG TGCCACATAT CCTTTACTTA ACCTAAGGAA CACAAAAAAT TTTCTACATA
481 TATCCTGGTT AGAGAGTGCT TAAAATAAGT TTTCCAAGAA TGGAAAAGAA ATGTTCTGAC
541 TTAACAATTA AGACAGTATT TATTTAAAGC AAGAAATATG AGGCACACAA GAAAATATTT
601 TGGGAAGAAA CCATTGGTG AACAATATTT CAAATAAAAA TAGACAAACA TAGTTAATTG
661 TAAACATAT GTTTGACCAG CCCTTCTTTT CAATAGGCTT AATGTGAATA AAATGTTAAA
721 GATTCTCTTT GGGTGGCTGC AAATTGTCCA CGAATAAGAC AAAATATAAA AATAAGGACT
781 GAGTCTCACA AAATGAAAAG GAAATATATT CAGAAAAGAGA ATCTTGAGAG AATGTGTTGT
841 CACAAATTAA AGAAAACCTG TGGTGAATGA CATCCTGAGG CCTGAGCTAT TACTGACATT
901 TAAGATAAAG GTAACGTGAT ACATTTGTCC CATTGAGGGG ACAAGAAAGC TGCTCTCATG
961 TTCAGCTCTA TAATCTTGC CTTAAACAAC TTAAATAGAA TGATTTAAAA TATGGAGCTG
1021 TCCATGGACC TTTGAAATAT AAAATAGTCA AGCAACTTAT CAAGGAATTA CAGATTCCTT
1081 GATACTAACA CAGGTAAATC CCACACGTGT TTTGAGACTA CATTTGCTGG GATTTTATTG
1141 ATGTAATAGG TCACATGTTT TTCGGGCCAA TGTTGCTGTT ATTCGGTTAC TTCAAGAGAA
1201 TAGTGGCAAC TGATGCTATG TATTCTAGGG GTTTGAAGTG ATGTTTCATG ATTGAAATTT
1261 GTAAAGAAT AACATCATCA TTCTTAACAA TAGAACATAT AAAGTCACAC AGAAGTGACA
1321 GTGTTTAAGC TGTACTATTG ATCAAAGAAA TTTATTACCT TCAGTTTCAA TGGAAATAAT
1381 TACTGATAAT ACAAACATGT GTGAACACAC ACTAATCCTA TCCAAATGCA CAGTGATACA
1441 CAGAAAATAT TAGCAAGTAG AATGCAATAT TTATATAACG ATTGTATTTA TCAATCAATT
1501 GTATGTATCA ATATATGGGC TATTTTCTTA CACATGATTT TATTCAAATT TACTCTAATC
1561 ATTGTTGAAC CATTTAGAAA AGGCATACTG GCAACTTTTC CTTACCTCAT CCAGCTGGGC
1621 AAAAGTCCCA GTGTGGAGTA AAGGATGCAA GATTTCTGTC TCTGTTAAGT ATAAAATAAT
1681 AGTATGAATT CAAAGGTGCC ATTCTTCTGC TTCTAGTTAT AAAGGCAGTG CTTGCTTCTT
1741 CCAGCACAGA TCTGGATCTC GAGGAGCTTG GCGAGATTTT CAGGAGCTAA GGAAGCTAAA
1801 AGCCGCCACC ATGAAAAGCCA TCTTAATCCC ATTTTATCT CTCTGATTC CGTTAACCCC
1861 GCAATCTGCA TTCGCTCAGA GTGAGCCGGA GCTGAAGCTG GAAAGTGTGG TGATTGTCAG
1921 TCGTCATGGT GTGCGTGCTC CAACCAAGGC CACGCAACTG ATGCAGGATG TCACCCAGA
1981 CGCATGGCCA ACCTGGCCGG TAAAAGTGGG TTGGCTGACA CCGCGCGGTG GTGAGCTAAT
2041 CGCCTATCTC GGACATTACC AACGCCAGCG TCTGGTAGCC GACGGATTGC TGGCGAAAAA
2101 GGGCTGCCCG CAGTCTGGTC AGGTGCGGAT TATTGCTGAT GTCGACGAGC GTACCCGTAA
2161 AACAGGCGAA GCCTTCGCCG CCGGCTGGC ACCTGACTGT GCAATAACCG TACATACCCA
2221 GGCAGATACG TCCAGTCCCG ATCCGTTATT TAATCCTCTA AAAAGTGGCG TTTGCCAACT
2281 GGATAACGCG AACGTGACTG ACGCATCCT CAGCAGGGCA GGAGGGTCAA TTGCTGACTT
2341 TACCGGGCAT CGGCAAACGG CGTTTCGCGA ACTGGAACGG GTGCTTAATT TTCCGCAATC
2401 AAACCTGTGC CTTAAACGTG AGAAACAGGA CGAAAGCTGT TCATTAACGC AGGCATTACC
2461 ATCGGAACTC AAGGTGAGCG CCGACAATGT CTCATTAACC GGTGCGGTAA GCCTCGCATC
2521 AATGCTGACG GAGATATTTT TCCTGCAACA AGCACAGGGA ATGCCGAGC CGGGGTGGGG
2581 AAGGATCACC GATTACACC AGTGAACAC CTTGCTAAGT TTGCATAACG CGCAATTTTA
2641 TTTGCTACAA CGCACGCCAG AGGTTGCCCG CAGCCGCGCC ACCCGGTTAT TAGATTTGAT
2701 CAAGACAGCG TTGACGCCCC ATCCACCGCA AAAACAGGCG TATGGTGTGA CATTACCCAC
2761 TTCAGTGCTG TTTATCGCCG GACACGATAC TAATCTGGCA AATCTCGGCG GCGCACTGGA
2821 GCTCAACTGG ACGCTTCCCG GTCAGCCGGA TAACACGCCG CCAGGTGGTG AACTGGTGT
2881 TGAACGCTGG CGTCGGCTAA GCGATAACAG CCAGTGGATT CAGGTTTCGC TGCTCTTCCA

```

Figure 19 (continued):

2941	GACTTTACAG	CAGATGCGTG	ATAAAACGCC	GCTGTCATTA	AATACGCCGC	CCGGAGAGGT
3001	GAAACTGACC	CTGGCAGGAT	GTGAAGAGCG	AAATGCGCAG	GGCATGTGTT	CGTTGGCAGG
3061	TTTTACGCAA	ATCGTGAATG	AAGCACGCAT	ACCCGCTTGC	AGTTTGTAAAG	GTATAAGGCA
3121	GTTATTGGTG	CCCTTAAACG	CCTGGTGCTA	CGCCTGAATA	AGTGATAATA	AGCGGATGAA
3181	TGGCAGAAAT	TCGCCGGATC	TTTGTGAAGG	AACCTTACTT	CTGTGGTGTG	ACATAATTGG
3241	ACAAACTACC	TACAGAGATT	TAAAGCTCTA	AGGTAAATAT	AAAATTTTTA	AGTGATAAAT
3301	GTGTTAAACT	ACTGATTCTA	ATTGTTTGTG	TATTTTAGAT	TCCAACCTAT	GGAACCTGATG
3361	AATGGGAGCA	GTGGTGGAAT	GCCTTTAATG	AGGAAAACCT	GTTTTGCTCA	GAAGAAATGC
3421	CATCTAGTGA	TGATGAGGCT	ACTGCTGACT	CTCAACATTC	TACTCCTCCA	AAAAAGAAGA
3481	GAAAGGTAGA	AGACCCCAAG	GACTTTCCTT	CAGAATTGCT	AAGTTTTTTG	AGTCATGCTG
3541	TGTTTAGTAA	TAGAACTCTT	GCTTGCTTTG	CTATTTACAC	CACAAAGGAA	AAAGCTGCAC
3601	TGCTATACAA	GAAAATTATG	GAAAAATATT	CTGTAACCTT	TATAAGTAGG	CATAACAGTT
3661	ATAATCATAA	CATACTGTTT	TTTCTTACTC	CACACAGGCA	TAGAGTGTCT	GCTATTAATA
3721	ACTATGCTCA	AAAATTGTGT	ACCTTTAGCT	TTTTAATTTG	TAAAGGGGTT	AATAAGGAAT
3781	ATTTGATGTA	TAGTGCCTTG	ACTAGAGATC	ATAATCAGCC	ATACCACATT	TGTAGAGGTT
3841	TTACTTGCTT	TAAAAAACCT	CCCACACCTC	CCCCTGAACC	TGAAACATAA	AATGAATGCA
3901	ATTGTTGTTG	TTAACTTGTT	TATTGCAGCT	TATAATGGTT	ACAAATAAAG	CAATAGCATC
3961	ACAAATTTCA	CAAATAAAGC	ATTTTTTTCA	CTGCATTCTA	GTTGTGGTTT	GTCCAAACTC
4021	ATCAATGTAT	CTTATCATGT	CTGGATCGAT	CCCCGGGTAC		

//

Figure 20: Nucleic acid sequence of the known segment of the R15/appa plasmid (including the vector sequences of pBLCAT3 (SEQ ID NO:4)).

LOCUS R15/appa 6116 bp DNA SYN 15-APR-2000
 DEFINITION R15/appa transgene with vector
 ACCESSION R15/appa
 REFERENCE 1 (bases 1 to 6116)
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequence.
 KEYWORDS salivary proline-rich protein, acid glucose-1-phosphatase; appA
 gene; periplasmic phosphoanhydride phosphohydrolase; artificial
 sequence;
 AUTHORS Golovan, S., Forsberg, C.W., Phillips, J.
 JOURNAL Unpublished.

DEFINITION Rat salivary proline-rich protein (RP15) gene.
 ACCESSION M64793 M36414
 VERSION M64793.1 GI:206711
 SOURCE Rat (Sprague-Dawley) liver DNA.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 1748)
 AUTHORS Lin, H.H. and Ann, D.K.
 TITLE Molecular characterization of rat multigene family
 encoding
 proline-rich proteins
 JOURNAL Genomics 10, 102-113 (1991)
 MEDLINE 91257817
 FEATURES Location/Qualifiers
 source 1..1748
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /tissue_type="liver"
 /tissue_lib="cosmid genomic library"
 misc_feature 1802-1810
 /function="consensus sequence for initiation in
 higher eukaryotes "

FEATURES Location/Qualifiers
 DEFINITION E. coli periplasmic phosphoanhydride phosphohydrolase (appA)
 gene,
 ACCESSION M58708 L03370 L03371 L03372 L03373 L03374 L03375
 VERSION M58708.1 GI:145283
 SOURCE Escherichia coli DNA.
 ORGANISM Escherichia coli
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia.

REFERENCE 1 (bases 1811..3109)
 AUTHORS Dassa, J., Marck, C. and Boquet, P.L.
 TITLE The complete nucleotide sequence of the Escherichia coli gene appA
 reveals significant homology between pH 2.5 acid phosphatase
 and glucose-1-phosphatase
 JOURNAL J. Bacteriol. 172 (9), 5497-5500 (1990)

Figure 20 (continued):

MEDLINE 90368616

FEATURES

Source	Location/Qualifiers
	1811..3109
	/organism="Escherichia coli"
	/db_xref="taxon:562"
sig_peptide	1811..1876
/gene="appA"	
CDS	1811..3109
	/gene="appA"
	/standard_name="acid phosphatase/phytase"
	/transl_table=11
	/product="periplasmic phosphoanhydride phosphohydrolase"
	/protein_id="AAA72086.1"
	/db_xref="GI:145285"

/translation="MKAILIPFLSLIPLTPQSAFAQSEPELKLESVVIVSRHGV RAP
TKATQLMQDVTDPDAWPTWPVKLGWLTPRGGELIAYLGHYQRQLVADGLLAKKGC PQS
GQVAIIADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNA
NVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPS
ELKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRI TDSHQWNTLLSLHNAQF
YLLQRTPEVARSRATPLLDLIKTALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGG
ALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIQVSLVFQTLQOMRDKTPLSLNT
PPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSL"

mat_peptide	1877 3106
	/gene="appA"
	/product="periplasmic phosphoanhydride phosphohydrolase"

mutation	replace(1817..1819,"gcg changed to gcc")
	/gene="appA"
	/standard_name="A3 mutant"
	/note="created by site directed mutagenesis"
	/phenotype="silent mutation"
mutation	replace(3092..3094," ccg changed to ccc")
	/gene="appA"
	/standard_name=" P428 mutant"
	/note="created by site directed mutagenesis"
	/phenotype=" silent mutation "
mutation	replace(3095..3097," gcg changed to gct")
	/gene="appA"
	/standard_name=" A429 mutant"
	/note="created by site directed mutagenesis"
	/phenotype=" silent mutation "

DEFINITION Plasmid pBLCAT3 (bases 3109 to 6116)

ACCESSION	X64409
VERSION	X64409.1 GI:58163
SOURCE	synthetic construct.
ORGANISM	synthetic construct artificial sequence.
REFERENCE	1 (bases 3109 to 6116)
AUTHORS	Luckow, B.H.R.
TITLE	Direct Submission
JOURNAL	Submitted (06-FEB-1992) B.H.R. Luckow, German Cancer Res Center, Im Neuenheimer Feld 280, W-6900 Heidelberg, FRG

Figure 20 (continued):

REFERENCE 2 (bases 3109 to 6116)
 AUTHORS Luckow, B. and Schutz, G.
 TITLE CAT constructions with multiple unique restriction sites
 for the functional analysis of eukaryotic promoters and
 regulatory elements
 JOURNAL Nucleic Acids Res. 15 (13), 5490 (1987)
 MEDLINE 87260024
 COMMENT Promoterless CAT vector for transient transfection
 experiments with eukaryotic cells. Allows the analysis of foreign
 promoters and enhancers.

FEATURES Location/Qualifiers
 source 3109 to 6116
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 polyA_signal 3262..3457
 /note="SV40 signals"
 CDS complement(4654..5514)
 /codon_start=1
 /transl_table=11
 /gene="Amp"
 /product="beta-lactamase"
 /protein_id="CAA45753.1"
 /db_xref="GI:58165"

BASE COUNT 1724 a 1386 c 1407 g 1599 t
 ORIGIN

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1 GGATCCCCTT TGCTATGTAG TTTTAAATGG AAATTACAAC CCATAGTGTG TTGATAAATA
61 GAGAGTCCTG TTTGGTTTAA GCAACCTCTG TTTCTCATAA ACTCCATAAA AACAGGAATA
121 CTCTTTGTTT CTAGCATAAC CAAAAGATTT AGTGAATTGA AAACAATGTT CCCTTAGAGT
181 ATAGGTCTAA TAACCCCGAA AATATTACCA TGATACTGAG CATTTGTAAG TATCTCATAG
241 CATGTAGTAT CCATAGTCCA TCAATGAGAG AGACATTTAA CATGATTTTC ATTAATCAGG
301 TGGAAAAGAC ATGACAACAT TCACAGGCAC TGCACAGAAC ATAGTGGTCC ACCTTGCACA
361 TATTTCACTA AACTAGGTTT ATCTATTTTG TTGCTTCTC TAACATCTCT GCAATGAAGC
421 AGGTCAACAG TGCCACATAT CCTTTACTTA ACCTAAGGAA CACAAAAAAT TTTCTACATA
481 TATCCTGGTT AGAGAGTGCT TAAAATAAGT TTTCCAAGAA TGGAAAAGAA ATGTTCTGAC
541 TTAACAATTA AGACAGTATT TATTTAAAGC AAGAAATATG AGGCACACAA GAAAATATTT
601 TGGGAAGAAA CCATTTGGTG AACAAATATT CAAATAAAAA TAGACAAACA TAGTTAATTG
661 TAAACATAT GTTTGACCAG CCCTTCTTTT CAATAGGCTT AATGTGAATA AATGTTAAA
721 GATTCTCTTT GGGTGGCTGC AAATTGTCCA CGAATAAGAC AAAATATAAA AATAAGGACT
781 GAGTCTCACA AAATGAAAAG GAAATATATT CAGAAAAGAGA ATCTTGAGAG AATGTGTTGT
841 CACAAATTAA AGAAAACCTG TGGTGAATGA CATCCTGAGG CCTGAGCTAT TACTGACATT
901 TAAGATAAAG GTAACGTAT ACATTTGTCC CATTGAGGGG ACAAGAAAGC TGCTCTCATG
961 TTCAGCTCTA TAATCTTGC CTAAACAAC TTAAATAGAA TGATTTAAAA TATGGAGCTG
1021 TCCATGGACC TTTGAAATAT AAAATAGTCA AGCAACTTAT CAAGGAATTA CAGATTCCTT
1081 GATACTAACA CAGGTAAATC CCACACGTGT TTTGAGACTA CATTGCTGG GATTTTATTG
1141 ATGTAATAGG TCACATGTTT TTCGGGCCAA TGTTGCTGTT ATTCGGTTAC TTCAAGAGAA
1201 TAGTGGCAAC TGATGCTATG TATTCTAGGG GTTTGAAGTG ATGTTTCATG ATTGAAATTT
1261 GTAAAAGAAT AACATCATCA TTCTTAACAA TAGAACATAT AAAGTCACAC AGAAGTGACA
1321 GTGTTTAAGC TGTACTATTG ATCAAAGAAA TTTATTACCT TCAGTTTCAA TGGAAATAAT
1381 TACTGATAAT ACAAACATGT GTGAACACAC ACTAATCCTA TCCAAATGCA CAGTGATACA
1441 CAGAAAATAT TAGCAAGTAG AATGCAATAT TTATATAACG ATTGTATTTA TCAATCAATT
1501 GTATGTATCA ATATATGGGC TATTTTCTTA CACATGATTT TATTCAAATT TACTCTAATC
1561 ATTGTTGAAC CATTTAGAAA AGGCATACTG GCAACTTTTC CTTACCTCAT CCAGCTGGGC
1621 AAAAGTCCCA GTGTGGAGTA AAGGATGCAA GATTTCTGTC TCTGTTAAGT ATAAAATAAT

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Figure 20 (continued):

5161	TCTTACTGTC	ATGCCATCCG	TAAGATGCTT	TTCTGTGACT	GGTGAGTACT	CAACCAAGTC
5221	ATTCTGAGAA	TAGTGTATGC	GGCGACCGAG	TTGCTCTTGC	CCGGCGTCAA	TACGGGATAA
5281	TACCGCGCCA	CATAGCAGAA	CTTTAAAAAGT	GCTCATCATT	GGAAAACGTT	CTTCGGGGCG
5341	AAACTCTCA	AGGATCTTAC	CGCTGTTGAG	ATCCAGTTCG	ATGTAACCCA	CTCGTGCACC
5401	CAACTGATCT	TCAGCATCTT	TTACTTTCAC	CAGCGTTTCT	GGGTGAGCAA	AAACAGGAAG
5461	GCAAAATGCC	GCAAAAAAGG	GAATAAGGGC	GACACGGAAA	TGTTGAATAC	TCATACTCTT
5521	CCTTTTTCAA	TATTATTGAA	GCATTTATCA	GGGTATTGT	CTCATGAGCG	GATACATATT
5581	TGAATGTATT	TAGAAAAATA	AACAAATAGG	GGTTCCGCGC	ACATTTCCCC	GAAAAGTGCC
5641	ACCTGACGTC	TAAGAAACCA	TTATTATCAT	GACATTAACC	TATAAAAATA	GGCGTATCAC
5701	GAGGCCCTTT	CGTCTCGCGC	GTTTCGGTGA	TGACGGTGAA	AACCTCTGAC	ACATGCAGCT
5761	CCCGGAGACG	GTCACAGCTT	GTCTGTAAGC	GGATGCCGGG	AGCAGACAAG	CCCGTCAGGG
5821	CGCGTCAGCG	GGTGTTGGCG	GGTGTCGGGG	CTGGCTTAAC	TATGCGGCAT	CAGAGCAGAT
5881	TGTACTGAGA	GTGCACCATA	TGCGGTGTGA	AATACCGCAC	AGATGCGTAA	GGAGAAAATA
5941	CCGCATCAGG	CGCCATTGCG	CATTCAGGCT	GCGCAACTGT	TGGGAAGGGC	GATCGGTGCG
6001	GGCCTCTTCG	CTATTACGCC	AGCTGGCGAA	AGGGGGATGT	GCTGCAAGGC	GATTAAGTTG
6061	GGTAACGCCA	GGGTTTTCCC	AGTCACGACG	TTGTAAAACG	ACGGCCAGTG	CCAAGC

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Figure 21: Nucleic acid sequence of the known segment of the R15/appa transgene used for the generation of transgenic mice (SEQ ID NO:5).

LOCUS R15/appa 3470 bp DNA SYN 15-APR-2000
 DEFINITION R15/appa transgene with vector sequences removed.
 ACCESSION R15/appa
 REFERENCE 1 (bases 1 to 3470)
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequence.
 KEYWORDS salivary proline-rich protein, acid glucose-1-phosphatase; appA
 gene; periplasmic phosphoanhydride phosphohydrolase; artificial
 sequence;
 AUTHORS Golovan, S., Forsberg, C.W., Phillips, J.
 JOURNAL Unpublished.

DEFINITION Rat salivary proline-rich protein (RP15) gene.
 ACCESSION M64793 M36414
 VERSION M64793.1 GI:206711
 SOURCE Rat (Sprague-Dawley) liver DNA.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 1748)
 AUTHORS Lin, H.H. and Ann, D.K.
 TITLE Molecular characterization of rat multigene family
 encoding
 proline-rich proteins
 JOURNAL Genomics 10, 102-113 (1991)
 MEDLINE 91257817
 FEATURES Location/Qualifiers
 source 1..1748
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /tissue_type="liver"
 /tissue_lib="cosmid genomic library"
 misc_feature 1802-1810
 /function=" consensus sequence for initiation in
 higher eukaryotes "

FEATURES Location/Qualifiers

DEFINITION E. coli periplasmic phosphoanhydride phosphohydrolase (appA)
 gene,

ACCESSION MS8708 L03370 L03371 L03372 L03373 L03374 L03375
 VERSION MS8708.1 GI:145283
 SOURCE Escherichia coli DNA.
 ORGANISM Escherichia coli
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia.

REFERENCE 1 (bases 1811..3109)
 AUTHORS Dassa, J., Marck, C. and Boquet, P.L.
 TITLE The complete nucleotide sequence of the Escherichia coli gene appA
 reveals significant homology between pH 2.5 acid phosphatase
 and glucose-1-phosphatase

Figure 21 (continued):

JOURNAL J. Bacteriol. 172 (9), 5497-5500 (1990)
 MEDLINE 90368616

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                                /standard_name="acid phosphatase/phytase"
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                                /product="periplasmic phosphoanhydride phosphohydrolase"
                                /protein_id="AAA72086.1"
                                /db_xref="GI:145285"

/translation="MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRA
TKATQLMQDVTTPDAWPTWPVKLGWLTTPRGGELIAYLGHYQRQLVADGLLAKKGCPQS
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NVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPS
ELKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQF
YLLQRTPEVARSRATPLLDLIKALTTPHPPQQAQYGVTLPTSVLFIAGHDTNLANLGG
ALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIVSLVFQTLQOMRDKTPLSLNT
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    mat_peptide                 1877..3106
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                                /product="periplasmic phosphoanhydride phosphohydrolase"

    mutation                    replace(1817..1819,"gcg changed to gcc")
                                /gene="appA"
                                /standard_name="A3 mutant"
                                /note="created by site directed mutagenesis"
                                /phenotype="silent mutation"
    mutation                    replace(3092..3094,"ccg changed to ccc")
                                /gene="appA"
                                /standard_name="P428 mutant"
                                /note="created by site directed mutagenesis"
                                /phenotype="silent mutation"
    mutation                    replace(3095..3097,"gcg changed to gct")
                                /gene="appA"
                                /standard_name="A429 mutant"
                                /note="created by site directed mutagenesis"
                                /phenotype="silent mutation"

    polyA_signal                3262..3457
                                /note="SV40 signals"

BASE COUNT      1065 a      721 c      735 g      949 t
ORIGIN
1  GGATCCCCTT TGCTATGTAG TTTTAAATGG AAATTACAAC CCATAGTGTG TTGATAAATA
61 GAGAGTCCTG TTTGGTTTAA GCAACCTCTG TTTCTCATAA ACTCCATAAA AACAGGAATA
121 CTCTTTGTTT CTAGCATAAC CAAAAGATTT AGTGAATTGA AAACAATGTT CCCTTAGAGT
181 ATAGGTCTAA TAACCCCGAA AATATTACCA TGATACTGAG CATTTGTAAG TATCTCATAG
241 CATGTAGTAT CCATAGTCCA TCAATGAGAG AGACATTTAA CATGATTTTC ATTAATCAGG

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Figure 21 (continued):

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301 TGGAAAAGAC ATGACAACAT TCACAGGCAC TGCACAGAAC ATAGTGGTCC ACCTTGCACA
361 TATTTCACTA AACTAGGTTT ATCTATTTTG TTGCTTTCTC TAACATCTCT GCAATGAAGC
421 AGGTCAACAG TGCCACATAT CCTTTACTTA ACCTAAGGAA CACAAAAAAT TTTCTACATA
481 TATCCTGGTT AGAGAGTGCT TAAAATAAGT TTTCCAAGAA TGGAAAAGAA ATGTTCTGAC
541 TTAACAATTA AGACAGTATT TATTTAAAGC AAGAAATATG AGGCACACAA GAAAATATTT
601 TGGGAAGAAA CCATTTGGTG AACAAATTTT CAAATAAAAA TAGACAAAAC TAGTTAATTG
661 TAAAACATAT GTTTGACCAG CCCTTCTTTT CAATAGGCTT AATGTGAATA AAATGTTAAA
721 GATTCTCTTT GGGTGGCTGC AAATTGTCCA CGAATAAGAC AAAATATAAA AATAAGGACT
781 GAGTCTCACA AAATGAAAAG GAAATATATT CAGAAAGAGA ATCTTGAGAG AATGTGTTGT
841 CACAAATTAA AGAAAACCTG TGGTGAATGA CATCCTGAGG CCTGAGCTAT TACTGACATT
901 TAAGATAAAG GTAACGTAT ACATTTGTCC CATTGAGGGG ACAAGAAAGC TGCTCTCATG
961 TTCAGCTCTA TAATTCTTGC CTTAAACAAC TTAAATAGAA TGATTTAAAA TATGGAGCTG
1021 TCCATGGACC TTTGAAATAT AAAATAGTCA AGCAACTTAT CAAGGAATTA CAGATTCCTT
1081 GATACTAACA CAGGTAAATC CCACACGTGT TTTGAGACTA CATTGCTGAG GATTTTATTG
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1201 TAGTGGCAAC TGATGCTATG TATCTAGGG GTTTGAAGTG ATGTTTCATG ATTGAAATTT
1261 GTAAAAGAAAT AACATCATCA TTCTTAACAA TAGAACATAT AAAGTCACAC AGAAGTGACA
1321 GTGTTTAAGC TGTACTATTG ATCAAAGAAA TTTATTACCT TCAGTTTCAA TGGAAATAAT
1381 TACTGATAAT ACAAACATGT GTGAACACAC ACTAATCCTA TCCAAATGCA CAGTGATACA
1441 CAGAAAATAT TAGCAAGTAG AATGCAATAT TTATATAACG ATTGTATTTA TCAATCAATT
1501 GTATGTATCA ATATATGGGC TATTTTCTTA CACATGATTT TATTCAAATT TACTCTAATC
1561 ATTGTTGAAC CATTTAGAAA AGGCATACTG GCAACTTTTC CTTACCTCAT CCAGCTGGGC
1621 AAAAGTCCCA GTGTGGAGTA AAGGATGCAA GATTTCTGCT TCTGTTAAGT ATAAAATAAT
1681 AGTATGAATT CAAAGGTGCC ATTCTTCTG TTCTAGTTAT AAAGGCAGTG CTTGCTTCTT
1741 CCAGCACAGA TCTGGATCTC GAGGAGCTTG CCGAGATTTT CAGGAGCTAA GGAAGCTAAA
1801 AGCCGCCACC ATGAAAGCCA TCTTAATCCC ATTTTATCT CTTCTGATTC CGTTAACCCC
1861 GCAATCTGCA TTCGCTCAGA GTGAGCCGGA GCTGAAGCTG GAAAGTGTGG TGATTGTCAG
1921 TCGTCATGGT GTGCGTGCTC CAACCAAGGC CACGCAACTG ATGCAGGATG TCACCCGAGA
1981 CGCATGGCCA ACCTGGCCCG TAAACTGGG TTGGCTGACA CCGCGCGGTG GTGAGCTAAT
2041 CGCCTATCTC GGACATTACC AACGCCAGCG TCTGGTAGCC GACGGATTGC TGGCGAAAAA
2101 GGGCTGCCCG CAGTCTGGTC AGGTCGCGAT TATTGCTGAT GTCGACGAGC GTACCCGTAA
2161 AACAGGCGAA GCCTTCGCCG CCGGGCTGGC ACCTGACTGT GCAATAACCG TACATACCCA
2221 GGCAGATACG TCCAGTCCCG ATCCGTTATT TAATCCTCTA AAAACTGGCG TTTGCCAATT
2281 GGATAACGCG AACGTGACTG ACGCGATCCT CAGCAGGGCA GGAGGGTCAA TTGCTGACTT
2341 TACCGGGCAT CGGCAAACGG CGTTTCGCGA ACTGGAACGG GTGCTTAATT TTCCGCAATC
2401 AAACCTGTGC CTTAAACGTG AGAAACAGGA CGAAAGCTGT TCATTAACGC AGGCATTACC
2461 ATCGGAACCTC AAGGTGAGCG CCGACAATGT CTCATTAACC GGTGCGGTAA GCCTCGCATC
2521 AATGCTGACG GAGATATTTT TCCTGCAACA AGCACAGGGA ATGCCGGAGC CGGGGTGGGG
2581 AAGGATCACC GATTACACAC AGTGGAACAC CTTGCTAAGT TTGCATAACG CGCAATTTTA
2641 TTTGCTACAA CGCACGCCAG AGGTTGCCCG CAGCCGCGCC ACCCCGTTAT TAGATTTGAT
2701 CAAGACAGCG TTGACGCCCC ATCCACCGCA AAAACAGGCG TATGGTGTGA CATTACCCAC
2761 TTCAGTGCTG TTTATCGCCG GACACGATAC TAATCTGGCA AATCTCGGCG GCGCACTGGA
2821 GCTCAACTGG ACGCTTCCCG GTCAGCCGGA TAACACGCCG CCAGGTGGTG AACTGGTGTT
2881 TGAACGCTGG CGTCGGCTAA GCGATAACAG CCAGTGGATT CAGGTTTCGC TGGTCTTCCA
2941 GACTTTACAG CAGATGCGTG ATAAAACGCC GCTGTCATTA AATACGCCGC CCGGAGAGGT
3001 GAAACTGACC CTGGCAGGAT GTGAAGAGCG AAATGCGCAG GGCATGTGTT CGTTGGCAGG
3061 TTTTACGCAA ATCGTGAATG AAGCACGCAT ACCCGCTTGC AGTTTGTAAG GTATAAGGCA
3121 GTTATTGGTG CCCTTAAACG CCTGGTGCTA CGCCTGAATA AGTGATAATA AGCGGATGAA
3181 TGGCAGAAAT TCGCCGGATC TTTGTGAAGG AACCTTACTT CTGTGGTGTG ACATAATTGG
3241 ACAAACCTACC TACAGAGATT TAAAAACCT CCCACACCTC CCCCTGAACC TGAAACATAA
3301 AATGAATGCA ATTGTTGTTG TTAACCTGTT TATTGCAGCT TATAATGGTT ACAAATAAAG
3361 CAATAGCATC ACAAATTTCA CAAATAAAGC ATTTTTTTCA CTGCATTCTA GTTGTGGTTT
3421 GTCCAAACTC ATCAATGTAT CTTATCATGT CTGGATCGAT CCCC GGGTAC

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Figure 22: Nucleic acid sequence of the SV40/APPA+intron plasmid (SEQ ID NO:6).

LOCUS SV40/APPA 5421 bp DNA CIRCULAR SYN 14-APR-2000
 DEFINITION Ligation of SV40 promoter/enhancer into CAT/APPA+intron
 ACCESSION SV40/APPA
 REFERENCE 1 (bases 1 to 5421)
 SOURCE synthetic construct.
 ORGANISM synthetic construct
 artificial sequence.
 KEYWORDS SV40 promoter/enhancer, acid glucose-1-phosphatase; appA gene;
 periplasmic phosphoanhydride phosphohydrolase; artificial
 sequence;
 AUTHORS Golovan, S., Forsberg, C.W., Phillips, J.
 JOURNAL Unpublished.

DEFINITION E. coli periplasmic phosphoanhydride phosphohydrolase (appA)
 gene,

ACCESSION M58708 L03370 L03371 L03372 L03373 L03374 L03375
 VERSION M58708.1 GI:145283
 SOURCE Escherichia coli DNA.
 ORGANISM Escherichia coli
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia.

REFERENCE 1 (bases 40 1337)
 AUTHORS Dassa, J., Marck, C. and Boquet, P.L.
 TITLE The complete nucleotide sequence of the Escherichia coli gene appA
 reveals significant homology between pH 2.5 acid phosphatase
 and glucose-1-phosphatase
 JOURNAL J. Bacteriol. 172 (9), 5497-5500 (1990)
 MEDLINE 90368616

FEATURES Location/Qualifiers
 Source 40 1337
 /organism="Escherichia coli"
 /db_xref="taxon:562"
 sig_peptide 40..105
 /gene="appA"
 CDS 40 1337
 /gene="appA"
 /standard_name="acid phosphatase/phytase"
 /transl_table=11
 /product="periplasmic phosphoanhydride phosphohydrolase"
 /protein_id="AAA72086.1"
 /db_xref="GI:145285"

/translation="MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAP
 TKATQLMQDVTPDAWPTWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQS
 GQVAIIADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNA
 NVTDAILSRAGGSIA DFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPS
 ELKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQF
 YLLQRTPEVARSRATPLLDLIKALTTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGG
 ALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIIQVSLVFQTLQOMRDKTPLSLNT
 PPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARI PACSL"
 mat_peptide 106 1334
 /gene="appA"

Figure 22 (continued):

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        /product="periplasmic phosphoanhydride phosphohydrolase"

mutation    replace(46.. 48,"gcg changed to gcc")
            /gene="appA"
            /standard_name="A3 mutant"
            /note="created by site directed mutagenesis"
            /phenotype="silent mutation"
mutation    replace(1320..1322," ccg changed to ccc")
            /gene="appA"
            /standard_name=" P428 mutant"
            /note="created by site directed mutagenesis"
            /phenotype=" silent mutation "
mutation    replace(1323..1325," gcg changed to gct")
            /gene="appA"
            /standard_name=" A429 mutant"
            /note="created by site directed mutagenesis"
            /phenotype=" silent mutation "

DEFINITION  Plasmid pBLCAT3  (bases 2200 to 4924)
ACCESSION   X64409
VERSION     X64409.1  GI:58163
SOURCE      synthetic construct.
ORGANISM    synthetic construct
            artificial sequence.
REFERENCE   1  (bases 2200 to 4924)
AUTHORS     Luckow,B.H.R.
TITLE       Direct Submission
JOURNAL     Submitted (06-FEB-1992) B.H.R. Luckow, German Cancer Res
            Center, Im Neuenheimer Feld 280, W-6900 Heidelberg, FRG
REFERENCE   2  (bases 2200 to 4924)
AUTHORS     Luckow,B. and Schutz,G.
TITLE       CAT constructions with multiple unique restriction sites
for
regulatory  the functional analysis of eukaryotic promoters and
            elements
            JOURNAL   Nucleic Acids Res. 15 (13), 5490 (1987)
            MEDLINE   87260024
            COMMENT    Promoterless CAT vector for transient transfection
experiments with eukaryotic cells. Allows the analysis of foreign
            promoters and enhancers.
FEATURES
    source   Location/Qualifiers
            2200 to 4924
            /organism="synthetic construct"
            /db_xref="taxon:32630"

    SV40 t intron  1380..1993
                  /note="SV40 signals"
    polyA_signal  1990..2230
                  /note="SV40 signals"
    CDS           complement(3471..4317)
                  /codon_start=1
                  /transl_table=11
                  /gene="Amp"
                  /product="beta-lactamase"
                  /protein_id="CAA45753.1"
                  /db_xref="GI:58165"

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Figure 22 (continued):

SV40 promoter/enhancer 5023..5402
/note="SV40 signals"

BASE COUNT	1413 a	1321 c	1331 g	1355 t	
ORIGIN					
1	CGAGATTTTC	AGGAGCTAAG	GAAGCTAAAA	GCCGCCACCA	TGAAAGCCAT CTTAATCCCA
61	TTTTTATCTC	TTCTGATTCC	GTTAACCCCG	CAATCTGCAT	TCGCTCAGAG TGAGCCGGAG
121	CTGAAGCTGG	AAAGTGTGGT	GATTGTCACT	CGTCATGGTG	TGCGTGCTCC AACCAAGGCC
181	ACGCAACTGA	TGCAGGATGT	CACCCCAGAC	GCATGGCCAA	CCTGGCCGGT AAAACTGGGT
241	TGGCTGACAC	CGCGNGGTGG	TGAGCTAATC	GCCTATCTCG	GACATTACCA ACGCCAGCGT
301	CTGGTAGCCG	ACGGATTGCT	GGCGAAAAAG	GGCTGCCCGC	AGTCTGGTCA GGTCCGGATT
361	ATTGCTGATG	TCGACGAGCG	TACCCGTAAA	ACAGGCGAAG	CCTTCGCCCG CGGGCTGGCA
421	CCTGACTGTG	CAATAACCGT	ACATAACCCG	GCAGATACGT	CCAGTCCCGA TCCGTTATTT
481	AATCCTCTAA	AAACTGGCGT	TTGCCAACTG	GATAACGCGA	ACGTGACTGA CGCGATCCTC
541	AGCAGGGCAG	GAGGGTCAAT	TGCTGACTTT	ACCGGGCATC	GGCAAACGGC GTTTTCGCGAA
601	CTGGAACGGG	TGCTTAATTT	TCCGCAATCA	AACTTGTGCC	TTAAACGTGA GAAACAGGAC
661	GAAAGCTGTT	CATTAACGCA	GGCATTACCA	TCGGAACTCA	AGGTGAGCGC CGACAATGTC
721	TCATTAACCG	GTGCGGTAAG	CCTCGCATCA	ATGCTGACGG	AGATATTTCT CCTGCAACAA
781	GCACAGGGAA	TGCCGGAGCC	GGGGTGGGGA	AGGATCACCG	ATTCACACCA GTGGAACACC
841	TTGCTAAGTT	TGCATAACGC	GCAATTTTAT	TTGCTACAAC	GCACGCCAGA GGTGCCCCG
901	AGCCGCGCCA	CCCCGTTATT	AGATTTGATC	AAGACAGCGT	TGACGCCCCA CCACCGCAAA
961	AACAGGCGTA	TGGTGTGACA	TTACCCACTT	CAGTGCTGTT	TATCGCCCGA CACGATACTA
1021	ATCTGGCAAA	TCTCGGCGGC	GCACCTGGAG	TCAACTGGAC	GCTTCCCGGT CAGCCGGATA
1081	ACACGCCGCC	AGGTGGTGAA	CTGGTGTTTG	AACGCTGGCG	TCGGCTAAGC GATAACAGCC
1141	AGTGGATTCA	GGTTTCGCTG	GTCTTCCAGA	CTTTACAGCA	GATGCGTGAT AAAACGCCGC
1201	TGTCATTAAA	TACGCCGCC	GGAGAGGTGA	AACTGACCCT	GGCAGGATGT GAAGAGCGAA
1261	ATGCGCAGGG	CATGTGTTCT	TTGGCAGGTT	TTACGCAAAT	CGTGAATGAA GCACGCATAC
1321	CCGCTTGACG	TTTGTAAGGC	AGTTATTGGT	GCCCTTAAAC	GCCTGGTGCT ACGCCTGAAT
1381	AAGTGATAAT	AAGCGGATGA	ATGGCAGAAA	TTCGCCGGAT	CTTTGTGAAG GAACCTTACT
1441	TCTGTGGTGT	GACATAATTG	GACAAACTAC	CTACAGAGAT	TTAAAGCTCT AAGGTAAATA
1501	TAAAATTTTT	AAGTGTATAA	TGTGTTAAAC	TACTGATTCT	AATTGTTTGT GTATTTTAGA
1561	TTCCAACCTA	TGGAAGTATG	GAATGGGAGC	AGTGGTGGAA	TGCCTTTAAT GAGGAAAACC
1621	TGTTTTTGCTC	AGAAGAAATG	CCATCTAGTG	ATGATGAGGC	TACTGCTGAC TCTCAACATT
1681	CTACTCCTCC	AAAAAAGAAG	AGAAAGGTAG	AAGACCCCAA	GGACTTTCCT TCAGAATTGC
1741	TAAGTTTTTT	GAGTCATGCT	GTGTTTAGTA	ATAGAACTCT	TGCTTGCTTT GCTATTTACA
1801	CCACAAAGGA	AAAAGCTGCA	CTGCTATACA	AGAAAATTAT	GGAAAAATAT TCTGTAACCT
1861	TTATAAGTAG	GCATAACAGT	TATAATCATA	ACATACTGTT	TTTTCTTACT CCACACAGGC
1921	ATAGAGTGTC	TGCTATTAAT	AACTATGCTC	AAAAATTGTG	TACCTTTAGC TTTTAAATTT
1981	GTAAAGGGGT	TAATAAGGAA	TATTTGATGT	ATAGTGCCCT	GACTAGAGAT CATAATCAGC
2041	CATACCACAT	TTGTAGAGGT	TTTACTTGCT	TTAAAAAACC	TCCCACACCT CCCCCTGAAC
2101	CTGAAACATA	AAATGAATGC	AATTGTTGTT	GTAACTTGT	TTATTGCAGC TTATAATGGT
2161	TACAAATAAA	GCAATAGCAT	CACAAATTTT	ACAAATAAAG	CATTTTTTTC ACTGCATTCT
2221	AGTTGTGGTT	TGTCCAAACT	CATCAATGTA	TCTTATCATG	TCTGGATCGA TCCCCGGGTA
2281	CCGAGCTCGA	ATTCGTAATC	ATGGTCATAG	CTGTTTCCTG	TGTGAAATTG TTATCCGCTC
2341	ACAATTTCCAC	ACAACATACG	AGCCGGAAGC	ATAAAGTGTA	AAGCCTGGGG TGCCTAATGA
2401	GTGAGCTAAC	TCACATTAAT	TGCGTTGCGC	TCACTGCCCG	CTTTCCAGTC GGGAAACCTG
2461	TCGTGCCAGC	TGCATTAATG	AATCGGCCAA	CGCGCGGGGA	GAGGCGGTTT GCGTATTGGG
2521	CGCTCTTCCG	CTTCTCTCGT	CACTGACTCG	CTGCGCTCGG	TCGTTCCGGT GCGGCGAGCG
2581	GTATCAGCTC	ACTCAAAGGC	GGTAATACGG	TTATCCACAG	AATCAGGGGA TAACGCAGGA
2641	AAGAACATGT	GAGCAAAAGG	CCAGCAAAAG	GCCAGGAACC	GTAAAAAGGC CGCGTTGCTG
2701	GCGTTTTTCC	ATAGGCTCCG	CCCCCTGAC	GAGCATCACA	AAAATCGACG CTCAAGTCAG
2761	AGGTGGCGAA	ACCCGACAGG	ACTATAAAGA	TACCAGGCGT	TTCCCCCTGG AAGCTCCCTC
2821	GTGCGCTCTC	CTGTTCCGAC	CCTGCCGCTT	ACCGGATACC	TGTCCGCTT TCTCCCTTCG
2881	GGAAGCGTGG	CGCTTTCTCA	ATGCTCACGC	TGTAGGTATC	TCAGTTCGGT GTAGGTCGTT
2941	CGCTCCAAGC	TGGGCTGTGT	GCACGAACCC	CCCGTTTCAGC	CCGACCGCTG CGCCTTATCC
3001	GGTAACTATC	GTCTTGAGTC	CAACCCGGTA	AGACACGACT	TATCGCCACT GGCAGCAGCC
3061	ACTGGTAACA	GGATTAGCAG	AGCGAGGTAT	GTAGGCGGTG	CTACAGAGTT CTTGAAGTGG

Figure 22 (continued):

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3121 TGGCCTAACT ACGGCTACAC TAGAAGGACA GTATTTGGTA TCTGCGCTCT GCTGAAGCCA
3181 GTTACCTTCG GAAAAAGAGT TGGTAGCTCT TGATCCGGCA AACAAACCAC CGCTGGTAGC
3241 GGTGGTTTTT TTGTTTGCAA GCAGCAGATT ACGCGCAGAA AAAAAGGATC TCAAGAAGAT
3301 CCTTGATCT TTTCTACGGG GTCTGACGCT CAGTGGAAACG AAAACTCACG TTAAGGGATT
3361 TTGGTCATGA GATTATCAAA AAGGATCTTC ACCTAGATCC TTTTAAATTA AAAATGAAGT
3421 TTTAAATCAA TCTAAAGTAT ATATGAGTAA ACTTGGTCTG ACAGTTACCA ATGCTTAATC
3481 AGTGAGGCAC CTATCTCAGC GATCTGTCTA TTTCGTTTCAT CCATAGTTGC CTGACTCCCC
3541 GTCGTGTAGA TAACTACGAT ACGGGAGGGC TTACCATCTG GCCCCAGTGC TGCAATGATA
3601 CCGCGAGACC CACGCTCACC GGCTCCAGAT TTATCAGCAA TAAACCAGCC AGCCGGAAGG
3661 GCCGAGCGCA GAAGTGGTCC TGCAACTTTA TCCGCCTCCA TCCAGTCTAT TAATTGTTGC
3721 CGGGAAGCTA GAGTAAGTAG TTCGCCAGTT AATAGTTTGC GCAACGTTGT TGCCATTGCT
3781 ACAGGCATCG TGGTGTACG CTCGTCGTTT GGTATGGCTT CATTCAGCTC CGGTTCCCAA
3841 CGATCAAGGC GAGTTACATG ATCCCCCATG TTGTGCAAAA AAGCGGTTAG CTCCTTCGGT
3901 CCTCCGATCG TTGTCAGAAG TAAGTTGGCC GCAGTGTTAT CACTCATGGT TATGGCAGCA
3961 CTGCATAATT CTCTTACTGT CATGCCATCC GTAAGATGCT TTTCTGTGAC TGGTGAGTAC
4021 TCAACCAAGT CATTCTGAGA ATAGTGTATG CGGCGACCGA GTTGCTCTTG CCCGGCGTCA
4081 ATACGGGGA ATACCGCGCC ACATGACAGA ACTTTAAAG TGCTCATCAT TGGAAAACGT
4141 TCTTCGGGGC GAAAACTCTC AAGGATCTTA CCGCTGTTGA GATCCAGTTC GATGTAACCC
4201 ACTCGTGCAC CCAACTGATC TTCAGCATCT TTTACTTTCA CCAGCGTTTC TGGGTGAGCA
4261 AAAACAGGAA GCCTAAATGC CGCAAAAAAG GGAATAAGGG CGACACGGAA ATGTTGAATA
4321 CTCATACTCT TCCTTTTTTCA ATATTATTGA AGCATTTATC AGGGTTATTG TCTCATGAGC
4381 GGATACATAT TTGAATGTAT TTAGAAAAAT AAACAAATAG GGGTCCGCG CACATTTCCC
4441 CGAAAAGTGC CACCTGACGT CTAAGAAACC ATTATTATCA TGACATTAAC CTATAAAAAT
4501 AGGCGTATCA CGAGGCCCTT TCGTCTCGCG CGTTTCGGTG ATGACGGTGA AAACCTCTGA
4561 CACATGCAGC TCCCGGAGAC GGTACACAGT TGTCTGTAAG CGGATGCCGG GAGCAGACAA
4621 GCCCGTCAGG GCGCGTCAGC GGGTGTGGC GGGTGTGCGG GCTGGCTTAA CTATGCGGCA
4681 TCAGAGCAGA TTGTACTGAG AGTGCACCAT ATGCGGTGTG AAATACCGCA CAGATGCGTA
4741 AGGAGAAAAT ACCGCATCAG GCGCCATTCG CCATTCAGGC TGCGCAACTG TTGGGAAGGG
4801 CGATCGGTGC GGGCCTCTTC GCTATTACGC CAGCTGGCGA AAGGGGGATG TGCTGCAAGG
4861 CGATTAAGTT GGGTAACGCC AGGGTTTTCC CAGTCACGAC GTTGTAATAAC GACGGCCAGT
4921 GCCAAGCTTT ACACTTTATG CTTCCGGCTC GTATGTTGTG TGGAATTGTG AGCGGATAAC
4981 AATTTACAC AGGAAACAGC TATGACCATG ATTACGAATT CGGCGCAGCA CCATGGCCTG
5041 AAATAACCTC TGAAAGAGGA ACTTGTTAGT GTACCTTCTG AGGCGGAAAG AACCAGCTGT
5101 GGAATGTGTG TCAGTTAGGG TGTGGAAAGT CCCCAGGCTC CCCAGCAGGC AGAAGTATGC
5161 AAAGCATGCA TCTCAATTAG TCAGCAACCA GGTGTGGAAG GTCCCCAGGC TCCCCAGCAG
5221 GCAGAAGTAT GCAAAGCATG CATCTCAATT AGTCAGCAAC CATAGTCCCG CCCCTAACTC
5281 CGCCCATCCC GCCCCTAACT CCGCCAGTT CCGCCCATTC TCCGCCCCAT GGCTGACTAA
5341 TTTTTTTTAT TTATGCAGAG GCCGAGGCCG CCTCGGCCTC TGAGCTATTC CAGAAGTAGT
5401 GAGGAGGCTC GAGGAGCTTG G

```

//

Figure 23. The nucleic acid sequence of the Lama2/APPA transgene used for the generation of transgenic mice and transgenic pigs (SEQ ID NO: 7)

LOCUS transgene 17732 bp DNA SYN 14-APR-2000
 DEFINITION Lama-appA cut XhoI..20623 to NotI..17732
 ACCESSION transgene
 KEYWORDS parotid secretory protein; acid glucose-1-phosphatase; appA
 gene;
 periplasmic phosphoanhydride phosphohydrolase; artificial
 sequence;
 cloning vector
 REFERENCE 1 (bases 1 to 17732)
 AUTHORS Golovan, S., Forsberg, C.W., Phillips, J.
 JOURNAL Unpublished.

FEATURES

DEFINITION M. musculus Psp gene for parotid secretory protein.

ACCESSION X68699

VERSION X68699.1 GI:53809

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 3777 to 5332;)

AUTHORS Svendsen, P., Laursen, J., Krogh-Pedersen, H. and Hjorth, J.P.

TITLE Novel salivary gland specific binding elements located in
 the PSP proximal enhancer core

JOURNAL Nucleic Acids Res. 26 (11), 2761-2770 (1998)

MEDLINE 98256451

REFERENCE 2 (bases 7147 to 12653; 13952 to 17731)

AUTHORS Mikkelsen, T.R.

TITLE Direct Submission

JOURNAL Submitted (07-OCT-1992) T.R. Mikkelsen, Department of
 Molecular Biology, University of Aarhus, CF Mollers Alle
 130, 8000 Aarhus, DENMARK

REFERENCE 3 (bases 7147 to 12653; 13952 to 17731)

AUTHORS Laursen J, Hjorth JP

TITLE A cassette for high-level expression in the mouse salivary
 glands.

JOURNAL Gene 1997 Oct 1;198(1-2):367-72

MEDLINE 9370303

FEATURES

Location/Qualifiers

source 1.to 12653; 13952 to 17731
 /organism="Mus musculus"
 /strain="C3H/As"
 /db_xref="taxon:10090"
 /chromosome="2"
 /map="Estimate: 69 cM from centromere"
 /clone="Lambda YP1, Lambda YP3, Lambda YP7"
 /clone_lib="Lambda-PHAGE (Lambda L47.1)"
 /germline
 /note="Allele: b"

misc_feature 3777-5332

/gene="PSP"

/function="salivary gland specific positive acting
 regulatory region"

enhancer 7147..8724

Figure 23 (continued):

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                /evidence=experimental
exon           11778..11824
                /gene="Psp"
                /note="exon a"
                /number=1
                /evidence=experimental
exon           12626.. 14190
                /gene="Psp"
                /note="exon b fused with exons h and i"
misc_feature   12644-12652
                /function=" consensus sequence for initiation in higher
                eukaryotes ."
misc_feature   13952-13965
                /function=" M13mp18 polylinker"

```

DEFINITION E. coli periplasmic phosphoanhydride phosphohydrolase (appA) gene,

```

ACCESSION  M58708 L03370 L03371 L03372 L03373 L03374 L03375
VERSION    M58708.1  GI:145283
SOURCE      Escherichia coli DNA.
ORGANISM    Escherichia coli
             Bacteria; Proteobacteria; gamma subdivision;
             Enterobacteriaceae;
             Escherichia.

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REFERENCE   1  (bases 12653..13951)
AUTHORS    Dassa,J., Marck,C. and Boquet,P.L.
TITLE       The complete nucleotide sequence of the Escherichia coli
             gene appA reveals significant homology between pH 2.5
             acid phosphatase and glucose-1-phosphatase
JOURNAL     J. Bacteriol. 172 (9), 5497-5500 (1990)
MEDLINE     90368616

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FEATURES             Location/Qualifiers
     Source             12653..13951
                        /organism="Escherichia coli"
                        /db_xref="taxon:562"
     sig_peptide         12653..12718
     /gene="appA"
     CDS                 12653             13951
                        /gene="appA"
                        /standard_name="acid phosphatase/phytase"
                        /transl_table=11
                        /product="periplasmic phosphoanhydride
                        phosphohydrolase"
                        /protein_id="AAA72086.1"
                        /db_xref="GI:145285"

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/translation="MKAILIPFLSLLIPLTPQSAFAQSEPELKLESVVIVSRHGVRAP
TKATQLMQDVTTPDAWPTWPVKLGWLTTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQS
GQVAIIADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNA
NVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPS

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Figure 23 (continued):

ELKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQF

YLLQRTPEVARSRATPLLDLIKALTTPHPQKQAYGVTLPTSVLFIAGHDTNLANLGG

ALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIVSLVFQTLQQMRDKTPLSLNT

PPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSL"

mat_peptide 12719 13948
/gene="appA"
/product="periplasmic phosphoanhydride
phosphohydrolase"

mutation replace(12659.. 12661,"gcg changed to gcc")
/gene="appA"
/standard_name="A3 mutant"
/note="created by site directed mutagenesis"
/citation={3}

mutation replace(13934..13936," ccg changed to ccc")
/gene="appA"
/standard_name=" P428 mutant"
/note="created by site directed mutagenesis"
/citation={3}

mutation replace(13937..13939," gcg changed to gct")
/gene="appA"
/standard_name=" A429 mutant"
/note="created by site directed mutagenesis"
/citation={3}

BASE COUNT 4719 a 4125 c 4168 g 4719 t
ORIGIN

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1 TCGAGAGTAT CTTTGTTCAGC TGTGCCTCCA ACAAAGGGGT ACTGTTGCCC ACATAGAAAG
61 ATCTAAACTA ATTAATTAAT CCCTCACCCG CAAATCTTTC AGTCACTAAG TTAGCACGAT
121 TGTGTAACAA GTTCTCCAAA GGAGAGATAC AGATGAGTGC GTATAGGGTG GACCTGGCTG
181 CTGAGGAGAC ACCTGCATCT GACTAAGAAG AGCCACGGTG TTAGTTGAAT GGTGTGGAGT
241 AGGGTGGTTC TGTGGGACAG TAGAAAATCG AGAGGCATGT GCCGTTTAGT GAACTGATGG
301 AAGCTACCCC AAACGACAGA GATTGTTCAGT CAGGCCAATC CGTTTCGAGT TTGATGGGCA
361 GCCGGACAGT GAGACAGACA CACCTACTCA GTTGGAGGAA GGATGAGAAC AATGGCCAGC
421 AGGGATTGAG AGACCCTGAC AGGCGCAAGG CCCTAACACA CACACCTACC ACCTCACTTG
481 ACAAAGCTGC CAAAGACCAA AGACTTGTTT TCCATTAGAA ATGACAGCTG GCTTGACCCG
541 ACAGCATAAT AAGCAGAGTG TACTCTGATT GGAGAACTTT AATGTGTTTC ATTCAGTATT
601 ATAAAAGGAC AGTATTACAG ATTTTGTTGT ACACTGCTGT TACATGTGGG GCAGTGTGTC
661 TTAAAGTAGG GTAAAGTACT CTTTAAAAAT GGGTCCTAGA TATTTTTTCC TTAACTCAA
721 GTCTCTTACT GTTTAAATGA TTTTATTTT GTTTAATATG GAGGAAAAAG AAGCGTAAAT
781 GGACAATATA TATTTAGAGA AAGATGGTTA GCTGTCAGAA AAATATGCAA ATCAAAATCA
841 CACCAAGACT GCAGCACACC CCTGTCAGAT GGCTGTGATC AAGAAAATAA ATGACAATGA
901 GTGGTGGTGA AGATGTACTA AAGGGAAACA CACACACACA CACACACACA CACACACACA
961 CACACTGGAG CAACCACTGT GGAAATCAGT ATGAATGGTC CTCAAAAACC TGAAGATAGA
1021 GCGGGGCGTG GTGGCATAACA CTTTATTTC CAGCACTGGG GAGGCAGAGG CAGGTGGATC
1081 TCTGAGTTCC AGGCCAGCCT GGTCTATAGC ACAGGTTCTA GGACAGCCAG GGCTACACAG
1141 AAAAAACCTG CCTTGATTAA ACCAAACCAA ACCAAACCAA ACCAAACCAA ACCAAACCAA
1201 ACCAAACCAA ACCAAACCAA ACCAAACCAA AACACTGAAG ATAGAACTTC AGTATTCCAT
1261 TCCTAGATAT ATACCCAATG GAGACTAAGT CAGCAAGACA CCTGCACAGC CATGTTCACT
1321 ACTACACTGT TCACCACAGC CAGGCTGTGG AACCAGCCTG AGTGTCCATG ATAAATGAAT

```

Figure 23 (continued):

1381	GGATAGGTAA	CTTCAAGGT	AAATGGACTC	TGCTGTGTAC	ATGCCTCACA	TTCTGTTTAT
1441	TCATTTTTCT	TTATGAGGTG	TCCATTCAGG	AGTCACATGG	TAGTTCTATT	TTCACTCTTC
1501	TGAAGATACT	ACACTGGTCC	CCACAGTTTA	CACTTTTATC	AGCAGTGAAT	AAGGGTTCCT
1561	CTATCCTTAC	CATCATTTGT	TGTAATTTTT	CTTGATGACC	CTCTTTCTGA	CAGGGATAGG
1621	ATGTAATATC	AGTGTGAGGA	AGTACAACCT	GTTTTCTAAG	TATTTATTGG	CCCCTTGCAT
1681	TTCTTCTTTT	GAAAACTGTC	GGTTCCTGAC	ATCTGCTCAG	GTATTCATTG	GATGTTGTTT
1741	CTTTGGTGTT	TGAGTTCCTA	TGAATTCCTAG	ATGTTAAATC	CCTGCCTGTG	GTTCTCTCCC
1801	ATTCTGTAGG	CTGCCTCCTC	ACCCTGGCAA	TTGTTGTCCT	TGTTTTGCAG	AAACTTTTGA
1861	CTTCATGGAA	TCTCATTTGT	CAGTTTTCCC	TCCTCTGCTA	TAGCCTGAGC	TAATGCACTG
1921	GTTTTTACAG	AGCCCTGGTC	TATGCCTTTA	TCCTCCTCTG	GCAGCTTCGG	AGTTTCATTT
1981	CTTACATTTA	GATCTTTGAT	CCACTTTGAA	CAAGTTTTGG	AGCAGGGTGA	GAGATACGAA
2041	TCTAGTTCCA	TTCTTCCATA	TGTGATCCTA	GTTTACATAG	CATCGTTGGT	TGAAGAGGTT
2101	TTATTTTATT	TTTAAATAAT	GTGTCATAAA	AAACGAGGTG	GTTGTAGCAG	TGTGGATTGG
2161	TTTCTTTGTC	CTTTGATCTA	CAGGTCCTGT	TTTGTGTCAG	TCTCATGATG	TTTTATTGCT
2221	ATGGCTCTGT	CATACAGTCT	GAGGTCAGGT	ATTGTGATAT	ACCTTCAGTA	TTGCTCCCTC
2281	AGACTCAGGT	TTGCTTTGGC	CAGGAGTCAT	CTTACTCAGT	GCTCTTAGAG	CTCCCCCAGC
2341	ATGTAGCTGC	TACTATTCTT	AGTTGATAAA	TCAGGAAACT	GGGGCTCAGA	GAGATTAACT
2401	GTCTTGAAGT	ACTTCTGGGG	AGGTGAAACG	TGGAGACACT	AAACTGTGTT	TACCCTGTAC
2461	TGCTCCAGTA	GCTGTCGGGT	GCTGGGCTAC	AGCAAAGCAC	CTATACTATA	TATTACTCAG
2521	GAGGTGGAAA	AACTCAGCCT	CCCTTGGGGT	TCCCAAGCTC	CCAGGTGTCC	AGTCACTGCT
2581	GGAAACCTCA	TGGAGTCTGA	AAGGAAGGGT	TGAGGGTACA	TGGGGCAGCG	ATGAGGAGCC
2641	TGGGGCTGGG	ATCTCCCAAA	CACCTGGATA	TCCAGATGCC	ACTGGGTCAG	GGGGAGTTGG
2701	GAACAGAGTT	GGGATGTCCA	TGGACCTGTG	ACAAGGCCAG	GGCCAGGGGG	AGGATAACTC
2761	TGGCTTTACT	AATTTGCGAA	AGTCCTTAGC	TTAGCAGCAG	TTGTCTGGGA	GCACAGAGGG
2821	GCCTTCTGTA	AGAGGCTCAG	GCAGTGCCCG	TCTGTAGGCG	AAGGTCTTCT	CCATGTTCCC
2881	CATGGTGGTT	CTTGATGAAA	GAGACAGTCC	TTGGCTCCAA	ACTGGTTTAT	TGATTGTTCA
2941	TTGTGGAAAA	TGGGTGCACA	CCACCTTCTC	AGGGTGGACC	AGAGATCAAA	TACCTTTTGC
3001	AGGGAGGAAT	ATCTGGGAAG	GGACGCTTAC	TGGCTAAACC	CTCAGGGCCT	CTAGATACAT
3061	CATTAGCATG	GAGAACTCTG	TTCTGGGCTA	CATGACCACA	GGCCACATTT	CCACAAGCCA
3121	CATGTGGGAA	GTGTGGCACA	TGTTCTAGGC	CAGGAATCTG	GTAGGGAGCG	TGGAGCCACC
3181	TACCATCCCA	GGTGGGTGCC	TGGGTGCCAG	GGACCCTGAA	CCCGCTCAAC	CTTACCAAGT
3241	TTCTTGGCAG	GGTCCACTGT	CCTACACAGA	AGCTGGAGGA	GGTGTGAGGG	TTGTGTCTTT
3301	GTGGAATGTC	CCATGCTGCT	TGGGGCTCAG	TTTCTCCACC	TGTACCTCAT	TGTTTGGGT
3361	ATAAAAAGTG	GGGATACTTT	ATTATTCTCT	GACTCGGTCC	TGAGGAAAAA	GATCTGTGGC
3421	AGTCCAGGAA	CCACACCCTG	AGGTTCTGCT	ACTGAAGGGA	CTCCCTAAGT	CTCTGGAGTC
3481	TCTCCCCCTC	ACAGAGCTGC	CAAAAGTCTAG	GTTCTTTTGA	GGATAACAGA	GCCATGCTTG
3541	GTAAGCAGAC	AACAGCATTT	GTTTACTCAA	CCTTCTTTTG	TCAGCTCCCT	CTTCATAAAC
3601	AAGTTGAGAC	ACCATGCTGG	CTTGAGGAAG	ACTTCTAAAG	CCAGACAACCT	GTGCAAGGAA
3661	GAAGAAGAAG	GGGCAAGTGG	AGTTAGCCTG	GATGTAGCCC	TCAAAGTCTC	CAGAGACCAG
3721	CCATGAAGGC	TCAAGTGGAG	GGCAAGACCT	GCAGCAGCCA	AGCATCTGGC	AGGAGAGGAT
3781	CCTGGGAACC	CCTCTACCAT	GACACACATT	CTTCCTGCAG	GTCACACTTA	ATAGGCCATT
3841	TCTTATTTGG	ATCTATCATG	GTGTTCTGTG	CGAGATTAAT	GAGGTGTTAT	GCTGCGAACA
3901	GAAAGTTATA	TAAAAACAAG	TCCCCCCCCC	TTGTCACTGC	TGCTAAGAAT	GTAGCAGAAA
3961	TTGTCTCAAG	TGTCTCTCTA	ATCAGAAACA	ATAAAGGTCT	CCTTGGATTG	AAGCCCTCCA
4021	GTTTCCTCCT	TCCTTGCTGA	GCCTTGGACA	CCCATACAAA	CCTCCTGGAT	GCTACAGCTC
4081	TGGGCAGAGA	CTCCAAGGTG	GGGAGTACT	GATGGTACAA	AAGCAAAATA	CTTGTTTGGG
4141	GGTACACCCA	CTCCTCTGCC	TGTGTGGTTC	CTGCAGTCAG	TCCTGCAGAC	AGGCCCTCAG
4201	TGGGTCTTCC	ATGGGCAACA	CGCAGAGGGA	GGCAATGGAT	GGGAATACCC	ACACCCTGGT
4261	TAGTTTACCC	CGGCCATGCT	CTCTGCTCTT	CATCCCTCCT	CTGCCCTCTG	CCACGGCTTT
4321	CTCTGCAGGA	ATCATATCTT	CATATTGGCC	CACAGGTGTT	CTCCTCACCC	TAGCTATGAT
4381	GTTTACTTTA	GAGTGACCTT	AGCAGGGCTG	GTGGGAATGA	GTTCTAGAAG	GCTCACGGAG
4441	ATGCTAGGGA	AGAAACGTCT	TCTAACTACT	GAGGTTACTA	AGTTCCTGGT	GGTTGTCTCT
4501	GCCTTTCCCT	TGTTAAAAGT	ACCTTGAAGT	TAGTGCAGAA	GAAATCAGAG	CCAGTCACA
4561	GAGTAAATAT	GGTCCTGAAG	ATTTCCTTTG	AGTGCCCAAG	ATCCATGACA	TTTCAAGAGC
4621	CCTCTTTGTA	CCTTAAGTCA	TTTGGGGTTG	TATCTTCTGC	TTGATGTATG	TGTGTGTGTT
4681	TATCAAAGAG	TGAGATGGTT	ACATAAGAGG	TGCTCTAAAG	GACAGAGAGG	ATTTGCAATT
4741	GTGGCATGTG	ACATCCTCAG	GCCTTGCTCT	GGTGCCAGGA	GGAAGTATG	CAGAAAAGAG
4801	TAAGAGGTCA	TTTCCTGGAG	GCTGTCACTA	TAGAGGAGAT	CTTAGAGTGC	ATTCCCTCCT

Figure 23 (continued):

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4861 CCAGGCCCTG CCTGAGGATA GACATGTGCT GACTGCAACT GAAACAGAGG CTTGGGATGG
4921 AGAGTTAGST TCACAGAAGG GAGGGTGGGA GATGGATGCT TGCTGGGTTC TGGGTCTCAT
4981 CACCAGCTCC TGACCACCCG GTCAGCCCAT GTGCTTATTC CATAGCTTTC TTTTGCTATG
5041 TTTACTCAGT GTGGTGTGTTG TTGGGACCCA GCAGAAGCCA GTCCCAGGCT GACAGCTGTG
5101 GATACACAGG GCAGCATGAG GGTCCCTCAGC CTGAAGCAGT CAGGCTGGCA GAAGAGAAAG
5161 ACCAGCACAC ATTCTTCAA CCAACTATGT CTTGAAAAAC AAACATATTA TATCACATAT
5221 ATTGCATTTA TGAGACAGCT AAAATGTACT CGGGTAGCAT GACTCCAGGT GGGGATATCT
5281 GCAAGTGCCA TGAGTGGCAG AGGGACAGCC AATGTGAGGC AAGAAGGAAT TCTGGCTCAA
5341 CACAGCTTAG CTCCCTGGTG TTGGTTCAAA CTTTGAGAGT TTGACCACAA GCACTTTTATT
5401 TTTGACATAT TTAAACAGAG CACAACCTTG GGAAAAAGTT TTCTTATGAA AATTATCACA
5461 ATAAAGCTTA AGGCATGACT ACATTAAAAT GCCTTTGCAA AGTATATGTG CCCTCTTCCA
5521 CAAGAATGGT TCTATTGACT GAGAAATAAT GTTCAGGATA AAGATCCAGG AAGAAAAGAT
5581 CAGGGATAAG TAAAATACTA AACTCTTTTG CAAAGTACAT AGACCCTCTT TCATAACAAT
5641 GGGTCTCTATT GACTGACAAG CACTGCTCAG GAGTTGGGAA AGAGTCTAGC ATAAGCACGA
5701 TAGCCTGGAG ACTCTAGTGA GGTCTAGTCT TACAGACAGC AAAAATCACC AGGTTACAAA
5761 CTACATTTCAT TTCCAGTTTT CTGATCAGGC ACAGGTATGA ATCCCTTCTG TTGAAGAGAA
5821 AAGTCCATGT GTTTAAAATA TCTGGTTTCT CCAGTGCTAT TAGCGAGAAG ACTTGAGCCC
5881 TATACAACCTC CCACCTGGAG TGACATCCTG TCTTCATGGT ATATTACATA CCTAGACACG
5941 CTCATCTCAC AGACTTAGGA CTTTGTCTTC TGATCTCCAT TTCTGATCCC ACTTCCACCT
6001 TTGCCTTGAT AGTGTCATTT TCTTCACTGC CTTGGTGACA ACCATGTTAT CCTCTGTGTA
6061 TTTGAGTGTT ACCATTTTCA GATTTTACCT GTATGCAAGA TCACACAGTC TTTGTCTTTC
6121 TGTCTGGATG CATGCTAATC TCTACACAAC AACCCTTCCC CGTCACTCAG ATCTTCTTCC
6181 ATTAACACAT ACATGGTGCT GAAGAGGCTA GGGAGCTTCC CTTAGTGGG GAGCTAGCTG
6241 GCTATTGGGC CTTTTTGACT GTCCAGGAAG GCCCCCAATT GCTGAGACAA GAACCTAGAT
6301 TCTTCATTAT TGACTCTAAC TCATGTATCA AGCAGAAGCT AATGAATAGT TATCAACAGG
6361 ATCAGAGGTT CCAGTGTAAG ACACCTTGAC ATGAAAGAAC GGAGGAAGGA CAGATGGATG
6421 CATAAAAGCA GGACCACTGC CCCAGGAAGG TCCTGGAAAC TGATGCAGGG CAAAGGACAG
6481 GTTATAAACC AAATCTTAGG GAGTCAGGAA GAGCACAGAG GAGCTCAACC AACTGACCAC
6541 TGCTTAGGGG CTACCAACCC AATCCTCCCT GTGGGAACAG CTAAGCTATC AGCCAAGGGT
6601 AATAAACAGG CAGGACCTGT GGATGACATG GAGAGCATAG GGACCCTGGG TCCAGCCTTT
6661 AGCACCTGCA CTCTCAGGAT ACTCCACCAT TGTGTCTTAG AGAGCCTAGG GATACTGGGT
6721 CCAGCCTTTG GTACCTTCAC TCTCAGGGTA CCCCATCACT GTGTCTTGA GAGCCTAGGC
6781 ACCCTGGGTC CAGCCTTCAG TACCTGCGCT CTCAGGACAC CCCACCATTG TCTCTTGCCC
6841 CGTCTCTTCT TCCTCTTCTT CCCTTTTCATT GTCTCTTCTC TGTCTCTTTC TTGACTCTCC
6901 TTTCCCTCA CACCCTCACT CTAGTTCTCC CCTTCCCTCT CTGCATCACC CTATTCTCTC
6961 TGTGTTCCCT CCACTTTTCT TTATCTCTCA TGCTTCTCTC CTCCCTCAAA TACTTGTAC
7021 CCACTATACT TCAGGGGCCA GCTCTAGTGA CAAAGCTGTT AATAGCAAGA CTCTCAGATC
7081 TCCAACGGCT CAGAGGAGCC AGACCCACCA AGAACTCTCT CCAGGTCCAA TTTAGGTTT
7141 CTTGAAAGC TTTCAGCAAA TGCTCAGGGA ACATGCCACT AACAAGAAGA TGCAAATTCC
7201 AGTTGAGAGT GGGAAAGGCC CTTGCGTAGG TCCCATCTTC CAGGCCAAGG TCAGAGGGGC
7261 TCTGTGTAAT CCGGATTGAC AGGGCTCAGA ACAATGTTTT GTTTTAAAGG TTTATTTATT
7321 TTAGGTGTTA GTGTCTTTGC TTGCATGACC TTATGTGCAT CATGTGTGTG CAGGTTTCTG
7381 ATGACAGTAG AGGAGGGCTT TGAATCCCTG GGGATAGGAA GTTACAGGAA ATTATAAGCT
7441 GCTTTGTGGG TCTTCTAGCT TTCCCAACAG AAGTGAATGC TCTTACCAC TGAGCCATCT
7501 CTCTAGGCCC AAGAGACATT GCTTTATGGA TATAATTGTG TGTGTGTGTC AACATTGAGG
7561 AAAGGGAAAT AAAAAAAAAA CTTAGCCGCG TAAGGTTGTA CAGTTTCACT AATTGCTACT
7621 TTTAGTTGTG ATAAAATGGC AGGTGCTTCA ACATTTATAT ATACAAAAAC TTCCCTGCTG
7681 GTGGTTCAAC TGTGAGAACT GGGGTAAGTG GGTGAGTTCT CTTTTTCTGT CTCTGTCTCT
7741 GTCTCTCTCC TTCCATTCTT TCTTAAAGGA AATAAACATT GCAGCTGGGT TATAGCTCAT
7801 CAATATGGAA GTTACAGAAG TGAAAAAAGG CATTGCCTTG GTGGGTGGTG TTACCAGCTG
7861 ATTTTTGGTT GTCCTGCAAG GAGGTCTGGG GACTGGCTGC TCTGTCTCTG TCTGTATGAG
7921 TGAGGGAAGT CTGGGGAGCA GATTCCCTAA CCTTCAGCCT GGCCTGGTTC CTGAGTGAAC
7981 CCAGCCTCTC TGGTCCTAGT AGCTTTTTC AAACAGGAAT CTGAGTGGTG ACAGGGAACA
8041 AGTACCAGCC CATTGCCTAA GTGCCAGGGT TAGTGAGGGC AGGAAGCTGC CATAGCTGGG
8101 ATTAGTAGTT GTATTGGATG TAGGAAGTCC TATCCTGGGA CAGCTAATCC TTAATGCTTC
8161 ACTGGAGATT TTCAATGAGA AATTTATCCC ACGGCCCATC TGGCCCCATC CTTTTGTCTC
8221 CAACAGCCAA GTATTTTCCA TTAGAGGAGA CTTCTGTAC ACTTGATGGA TGCTCATTC
8281 AAGGTGACTT GGGGCAGTCA GTACAGACTT GGGATGACCT CTGACAGGCT AACCTCTCCC

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Figure 23 (continued):

8341	CAACAAGGGC	CCTCTATGTT	TGCTATGTAA	TGTAATGTCA	GACATTGTCA	GGAGTGTCCC
8401	CAGCACAGCC	TGCCCAGTGT	GAGGGCTCTC	ATAGGTTTCC	CACTGTCTTA	TCTACACAGG
8461	GATAACGAGG	AGGTAAGCTG	CAGTTCCAG	TCTCACTTCA	CAGAGGAAGA	GATAACCCCA
8521	TCCCAGGTCA	TGTAGCCAGC	AGTGGAAGA	ATGAGGATTT	GAACCTCAGT	CTTCCAAGTC
8581	CCATTGATAG	CATCTCCTCA	CAAGTCCCTT	GCCACCCTCA	CGATGCCTTA	GACACTTGCC
8641	TGCCCTTTAT	ACTAAGGAGA	TGCAGGTACA	AGGGGTTTAC	CCATGTAGCA	GCTGAGGCAG
8701	CTGGGGATAG	ATACCAGCAG	CAGGCCTGAT	GTCACCACTC	TAACCTCCAGC	ATCCCCAGTC
8761	TGTGTTCCCTG	GAGTGTGAAA	ATCCCTACTT	AACAAGATTG	TGCAACAGTC	CTTGCTCTG
8821	TGACCCATAG	CTGGAAACAG	GATTCTCATT	GATTTGTGGA	ACATGGTGGC	AGCCAGCCAA
8881	AAAGAGGGTC	TGCATACAGA	AGACACGTGT	GGCAAGGCCA	CAGCAGACTC	TGACTACCTT
8941	AGCTTACAGA	ATTACAAGGT	CATAATGTCC	TCTGCTTTGG	TCACCTCATG	TTAAGGACAG
9001	GCCCTAATGA	AGATGGGGCA	GAAGACTGAA	GGAATGGCCA	ACCAATAACT	GGCCCAACTT
9061	GAGACCCATC	CTACAGGCAA	GCATCAATTC	CTGACACTAC	TAATGATACT	CTGTTATGCT
9121	TGCAGACAGA	AGCCTAGCAT	AACTATCCTC	CGAGAGGTCC	ACCCAGCAAC	TGACTGAAAC
9181	AGAAAAAGAT	ATCCACAGGC	AAACAGTGGG	TGGAGGTCAG	GGACTATTAT	GGGAGAGCTG
9241	TGGGAAGGAT	TAAAAACCTT	GAAGGGGATA	GGAACCCAC	AGGAAGACCA	ACAGAGTCAA
9301	CTAAGAGACC	TGTGGGAGCT	CTCAGAGACT	GAGCCACCAA	CCAAAGAGCA	TACACAGGCC
9361	GGTCCGAGGC	ACCTGGCAGC	TGTGAAGCAG	ACATGCAGCT	CAGTCTCCAT	GTAGGTCTCTC
9421	CAATAAGCGG	TAGCCTGACT	GCAGTATCCA	ATCCCCAACA	GGGCTGCATA	GTCTGGCCTC
9481	AGTGGGGGAG	GATGCCCTTA	ATCCTGCAGA	GACTTGATGA	GTGGAGAGCT	ATCCAGGGGG
9541	AACCCACCCT	CTCTGAGAAG	GGAATGGGGA	TGGGGGAGGG	ACTCTGTGAA	GAGGGGACAA
9601	GGACAAACAA	GAACCTCAAA	TAGGTCAGGC	CCTAAAGGCT	TGCTAAGTAG	CAGTGGCCCA
9661	GCTCTGTCTT	GTTCTCTCAGC	CCAAGGCTCA	GCTCCACCT	GTTTCTGTGT	TTTTCTGGCT
9721	TTTCATGGGC	CTAGGACTTG	GTGACCAGTT	CAACAATGG	GGCCTGTGGA	AGACACAATA
9781	TACAAGACTA	GGGACATTCC	TGTTCTGCTG	ACTATCCATA	GCCTGATGTA	GGTGGAAGGA
9841	CCCAATCACT	GGATTCTTAC	CCTTGACAAA	CCTTGACAGC	TGAGGGCCTC	TCAGAAACCT
9901	ATTTCTTCCA	CTGAAAAATG	AGACTCTCAA	ATGAACGTCG	TGACAATCAT	CAGGCTTATT
9961	AAAGAGGTGT	ATCTAACCTG	AATGGCAAGC	AGACAGCAGG	CAAATGTCTG	TATCAACCTC
10021	TAGGAAGGAC	AAGAACTGCT	CACTGCTGCC	CCCCAGGAGG	CCATTTGCTG	AAACAGCTGC
10081	TCTCCTGCTG	GTGCACAGGC	CCTGCCTTCT	CATTGCAGCC	ACAGCCCCTT	CCTGTCTGAA
10141	CCTCCTGTCA	GGTCACTGGG	AAACAGATCA	AGATGGAACA	GGACAGCTCC	TGATGGTAAA
10201	TAAAAAACAG	TGGTCATGGC	TATTCATAGG	GGTTTATGCT	TCTTCAGTCC	ACACTGTGAA
10261	GAGCTGTGGG	CATGAACCAC	AGTGTTCGAG	GTAGAGTTGG	GGTTCTGAAA	TTACAGTGG
10321	GGTGAGCTCA	GTAAATGTGA	GCTGGAGGTC	ACTCGTGAGA	CACACAGTCC	TGCTGCTTCT
10381	GTTCCCAATA	TCCTGAGGAG	ACGACACATC	TACTTTGTTC	AGAGGCCACA	GTCTAGTTGA
10441	CCTGAGAGTT	ACCAGTTTCT	TATTTGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG
10501	TGTTGTTCCG	GTGTGAGTGC	AGGTGCACAT	ATGATAGCGT	ACACGTTGAG	GTCAGAGGAT
10561	AACTATCAGG	CGTTGTCCCC	TCCTACTTTT	CCTCGGACTC	TGGAGAACAA	ACATGGSTCC
10621	TTATTCCAGG	GGAGCAAGTC	GCTGTTGGCT	GACACATCTT	GCTCACATAC	ATTTTACCTA
10681	GACAATGGAG	CCTCCATCAG	AGTATTACTT	TAGCTCCTCA	CCGATGGCAA	TGCACCACCT
10741	CTCTACCCAC	ATAGGAGTTG	GGTCTCCACA	CACCCCCACA	CCCCCTTCAC	CAAAACGTTT
10801	TCAGTTACTT	TATCTGGTAA	AGTTCATCAG	AGAATGAAGC	CAGTATTAAG	AACATGGAAT
10861	CATTTGGGAA	CCTGGATCTA	GCAATACCCG	ACCCTAGATG	GAGTTGCTGA	GTTTTACCTT
10921	CAGATTATAA	TTCCCCCCTA	GCTTCTATGG	TTTATTCTGA	AACCAGGGGA	ACTCGATTCC
10981	TCCCTTTGGA	CCACAGACAT	CCTGGCTTGT	GAATTCACAT	GTCATCTACT	GCTAATCCAT
11041	TGGTAGTATG	TGGCTCACAG	AGACACACTA	CAGTCATGGC	CAATGTCAAG	GTAGGACAGA
11101	TGTGAATCAT	TCCCCCAGTC	CTGCTGTTTT	CATGACTAAC	CCTCCTCAGC	ACAGTGACCA
11161	TGAACCTACT	TTTCCCCCTC	TTTTATTTTT	AGAATTGCTG	GAATTTTCTA	TTTTGAGAAA
11221	TAATAGCCTT	GGGCAGCATT	AAACAAAATC	ATCTAGAAAG	CTGGTTTAAA	ATACAGATGG
11281	TTGAGTCAGT	GAAAGAGTGA	GGAATGTCAT	TATTGGCCCC	TCACAGAGGC	TGGCTCACTC
11341	CAGCAGAGGT	GGTTGAAGCT	CTTGGACACG	GGTCAGGTGC	ATAGGAAAGG	TNGTCTGGGA
11401	CACTGAGAAC	CACAATTGAA	CAAAACAGAA	TGTTGGCTTT	TTTTTTTTTA	AATGAGTTCT
11461	CAAAAAATGA	CTGGCTAGCT	TAGGCCAATA	CTTCGAGCCA	ACCCAACAGA	ACATTCTTCC
11521	ATTGATTTCAT	TCTGGATCTT	CTTTCTAGAC	AATACTGAAC	TGACCCCTTG	TTGGCAGTCT
11581	CAAGTTTGAC	AACATAGGGC	TTTGAACCTG	GCACAAGGTC	CATCACTGTC	ACCCAAGCAT
11641	CCTGGGTGAC	CTTTGGGTTG	GAATATCTTG	GCTAACCTTA	GATATTTTCT	TTGGAGTATC
11701	TTTAGAACAT	CCAGGAAATA	GGGCTTGATT	CTCATCCTGG	GACCACAATA	TAAGTCACCC
11761	TAGAATCCCA	GGAGATCGTG	CAGAGAAACA	AGGATCTCTC	TCGTGTGCA	CCTTCTTCAA

Figure 23 (continued):

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11821 AGCAGTGAGT AGTGA CTAAACTGAG TTCCCATCTG AGAGTCCACA GGAGGCTTTG
11881 GGGCAAGAAG CAGAGGGAAG GCACTGTTTG TGTGGTAA GTTTTGACTC TAACAAATTT
11941 GAAGACATAG ATGACATTGT GTCAGACTAA CAACAACCTA GACTCATGTG GGTTCTGTTT
12001 AGGGATCAGA TTTTATTCAT CAATGACTTG TCTTAGTGTA TAGAGAAAGG CTTCTACTG
12061 GAGTGTAGGC TCAATAATGA CAGAAGAGAT AGCTATTTCC CCTAGGGACT GTGCTGCTCC
12121 AAGTTTGGTG GAGAAAGGCA GTGGGGAACC TAGATGTGCT CTCTGGGGAG GGGGTCTGAA
12181 GCTGGCTTCA TAGAAGGTGT GAAGTTTTCG TGAAACATCT AAACAGAATT ATAGCTTAGG
12241 AAAGTGAGCA GGCAAGGCAG GGAATGTGTT GCATATGTAT ATGTACATGA ATATATTATG
12301 TTATAGATAC ACACACATTT GAACCTCATT TGCAGATGAC AGAAAATAGG TTATTTTGCC
12361 TCTCTTAAC TCTAAGCACA ATGACTTCCA GTTCCATCCA TTTCCTGAAA TGCCACAATT
12421 TCATTTTTCA TTGTGGCTGA ATAAAATTCC ATTGCAGACT GGGCCCTACT TCATCCACTC
12481 CTGAGGGCAG GCATATCCCC TGGCTCCATT TCTTACCTAT TGTGAAGAGA AGTGCACATG
12541 TCTTGTTGAA AGGCAAGCGT GAGAGAGGCA GGCCTAATT GTGGGTTTTT GTTCTTCTT
12601 CCTGCTATGA CTCTCCATT GTGAGAACCA AAGATCGATA AAAGCCGCCA CCATGAAAGC
12661 CATCTTAATC CCATTTTTAT CTCTTCTGAT TCCGTTAACC CCGCAATCTG CATTGCTCA
12721 GAGTGAGCCG GAGCTGAAGC TGGAAAGTGT GGTGATTGTC AGTCGTCATG GTGTGCGTGC
12781 TCCAACCAAG GCCACGCAAC TGATGCAGGA TGTCACCCCA GACGCATGGC CAACCTGGCC
12841 GGTAAGACTG GGTGGCTGA CACCGCGCGG TGGTGAGCTA ATCGCCTATC TCGGACATTA
12901 CCAACGCCAG CGTCTGGTAG CCGACGGATT GCTGGCGAAA AAGGGCTGCC CGCAGTCTGG
12961 TCAGGTGCGG ATTATTGCTG ATGTCGACGA GCGTACCCGT AAAACAGGCG AAGCCTTCGC
13021 CGCCGGGCTG GCACCTGACT GTGCAATAAC CGTACATACC CAGGCAGATA CGTCCAGTCC
13081 CGATCCGTTA TTTAATCCTC TAAAACTGG CGTTTGCCAA CTGGATAACG CGAACGTGAC
13141 TGACGCGATC CTCAGCAGGG CAGGAGGGTC AATTGCTGAC TTTACCGGCG ATCGGCAAAC
13201 GGC GTTTCGC GAACTGGAAC GGGTGCTTAA TTTTCCGCAA TCAAAC TTGT GCCTTAAACG
13261 TGAGAAACAG GACGAAAGCT GTTCATTAAC GCAGGCATTA CCATCGGAAC TCAAGGTGAG
13321 CGCCGACAAT GTCTCATTA CCGGTGCGGT AAGCCTCGCA TCAATGCTGA CGGAGATATT
13381 TCTCTGCAA CAAGCACAGG GAATGCCGGA GCCGGGGTGG GGAAGGATCA CCGATT CACA
13441 CCAGTGGAAC ACCTTGCTAA GTTTGCATAA CGCGCAATTT TATTTGCTAC AACGCACGCC
13501 AGAGGTTGCC CGCAGCCGCG CCACCCCGTT ATTAGATTTG ATCAAGACAG CGTTGACGCC
13561 CCATCCACCG CAAAAACAGG CGTATGGTGT GACATTACCC ACTTCAGTGC TGTATTATCG
13621 CGGACACGAT ACTAATCTGG CAAATCTCGG CGGCGCACTG GAGCTCAACT GAGCGTCTCC
13681 CCGTCAGCCG GATAACACGC CGCCAGGTG TGAACGCTG TTTGAACGCT GGCCTCGCT
13741 AGCGATAAC AGCCAGTGGA TTCAGGTTTC GCTGGTCTTC CAGACTTTAC AGCAGATGCG
13801 TGATAAAACG CCGCTGTCAT TAAATACGCC GCCCGGAGAG GTGAAACTGA CCCTGGCAGG
13861 ATGTGAAGAG CGAAATGCGC AGGGCATGTG TTCGTTGGCA GGTTTTACGC AAATCGTGAA
13921 TGAAGCACGC ATACCCGCTT GCAGTTTGTA AGGTACCCGG GGATCACAAC TTGCCCTCTG
13981 AAGAGGAAGA ACAGAAGGAT GCCACAATC TCCTGCTGGC TACTCTCCAG TGGTTTCATC
14041 TTACTTCTGA TGGCATTTC CTCTAGAAAG TGCTACTATC ATCCACACAT TTCTACCTGA
14101 GACCACCCAA AGGACCCTCC CAAATCTCT TCTCTCTGA GTAGTCTCCA CACCTGTTAC
14161 CACCATCCCA GAATTAATA CCTAACTGCA CTCTGGCGTG TGACTTGCTT CAGTCTTGC
14221 AATAAGAGTT GTTGGCAGTG CCAGGCGTGG TGGCGCACGC CTTTAATTC AGCACTTGGG
14281 AGGCAGAGGC AGGCGGATTT CTGAGTTCTGA GGCCAGCCTG GTCTACAGAG TGAGTTCCAG
14341 GACAGCCAGG GCTATACAGA GAAACCCCTGT GTCGAAAAAC CAAAAAAGTT
14401 GTTGGCAGAG TGTGGGTTAT ATACCAGGTG GAGATTTCAA ATGAGTGGCT GAAGCTGTAG
14461 CCAGAAGGAA CTTAGAGGAT AGCTCATAAC TTAAAAAGAA ATGTAGAGAG TAGCAGAAAC
14521 ATTGAGAGAG TGGGCACACA GCCACTGTGT GAATGTGGCA GAACACAATC CAGCCAGCTA
14581 TACATGCATA AGTGTATATT GGCGCCATCC TGAATGATGA GACACAGGAA AACAGATAGA
14641 CGGGGTTAGG TGGCCATGGC CTTTCTTGCC TGCTCTTCC TAAGGGTCAT CTCAAGACCT
14701 TATGCTCTCT TAACCTTCC ATTGCTACTT AGCTTCTAGA TATCACCTCC AGATTAGTCT
14761 CCTTGGGTAC ATCAGTGATC CTGGTGATAT CCAGGGCTTC CTGATTCCAT CTTTGTCTA
14821 GAGGCTGCAA CTAAAGAGGT TTTCTTAATA CTTACACACC TGATGCCAAA AGGAAGACAC
14881 AGAAGTTCAC AGAGGTGAAG GTATTCAATG AGGACATACA GTGAGCAAGC ATCAGGGTCC
14941 GGATTATCTG ACTCTACTCT AACTTTTATG TAAATGTGCT TTATGCCATT AACACTGTCA
15001 TTCCTGTGCT TCAGCTCTGG GAGACTCCCA AGCACTCTTA GGCACAAGCC ACAATTAAGG
15061 GACTCTGACA CTCTGCATTG ATTAATTAGC ATGGTGGTCT CTATGTTTCC AGATTCATGA
15121 TTGTTTCACT TTCCATATAG GCTATGAAGG GTGTGAGGAA ATTTTGTGG GACAGAATTG
15181 GAGGCAATCC ACCTCTCTCA GGAAGCCTCT ATCTGGAAAA GCTTACAACT CAGGGACAGT
15241 AACTGTAGGC CCAGTCCTTG GTGTCCAAAA TGGGTTTTAT GGTTTGAATC TGCAAAGCCT

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Figure 23 (continued):

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15301 TCCATGTGCT CAAAGGTTTG AACATGGAGC CTCCTCCTGG TAACACTGTA TTGGAGGCTT
15361 TTGAGACTGG ATGCTCTTTG GTCCCATGTT TTGCTACATC ATCTGTCAAG ATATGACCCA
15421 GGCATGCTAC CAGCTACCAC AGACTATGCC TCTCCAGCTT TCATGTTCTC CCCACCATGA
15481 TAGACTTGTA TCTCCTAAAA ATGGAATCAA AGCAAACTTT TCCTGCATTA AGTTTTTTTT
15541 TTTCTGTTAA GTGTTTGGTC ACAGGGACAA GAAAACACTC AATACAGATA ATTAGTACCA
15601 GAGTTGAGGT TCATTGCTCT AGCAAGTTGG ATCAAATTTT TAGGGCTTTG GAACTGATTT
15661 ATAAGAGACA TGTAAGAGAG TCTGAAGCTG TGGGCTACAG AAGTGTCAAC AGTTTTTAAG
15721 AATAGTTTAA TACACCATGG GAATTGTGAA AATCAGAATG CTCACACAAA GGCAGACAGG
15781 AAAACGTGAG CATGTGGCGT GTGAGAGGGC ATAAGAAGGA ACCTAGGGGG AAATGAGCTA
15841 GAAGCCATTC GGCTACGTTA GGGAACGTGT GTGGCTGTGC TTGGCCCATG CCCTGGCAAT
15901 CTGAATGAGG CCAAATTTTA AAGGAGTGGA CTAACCTCGAT TGTCAGAGAA AATATCAAGA
15961 CAGACCACCA CTCAGGCTAT GCCGTGTTTG TGACCGACCA GCTACTCTTA GCCAGCTCTA
16021 TTGTGAAATT CCAGAGCAAT TATCAGAGCA TGAAGATACA TACAGTTTAG TGAAGTAAGG
16081 GGTGTGGGTC CCTAAGTGGA TGGTGCAATA ATCTATGTAG GTGATGCCTA AGTGACACTT
16141 GATAATCCAA AATATCAGCA ATGTGGAATG TCTTCCAAGG AGACCTGTAG ACACACATTT
16201 TAGAACTTTG CTCATGGCTG TAATAAATAG CTAGCTAGAA ATCATTTTCT GAAGAGGTTA
16261 GTCTGAGTTA CGGTTCCAGG GCAAACATTC AGTGATGGCA AGGAAGGCAT TGCAGTCAGG
16321 AGCCAAAGGT CAGCTGGTCA CATTGCATCA AGAGTAGAGA GTCAGAGTGT GAGTAGAAAG
16381 AGGATACAGG TTATAAAACC TCACTGTCCA CTCTCAGCAA TCCATTTTCT CCTAAAAGGC
16441 TTTACCTTCT AAAGATTTTA GTCTTCAAAA CCAGTACCAG TAGCCTGGGA ACAAAGTTG
16501 AAACAAATGA GCCTTTGTGG GGCATTTTAC ACTTAAACA GGGCATCACC TAGGAGGAGC
16561 CCTGTGTGCA GTAGGAAGTG TGGCCTCTGT GTCAGGAATG CTCAGGCTAA TAAGGGGTCC
16621 TCTATCTGAG GGACCCTATG AAGATTCAAC AAGTAGTTGT GAGAATTCCC TGTAAATGGA
16681 TGCTACCAAT TTGACATTTG TAGACCTGCT ATTGTGTGCT TCTTTATTGG GCTCTCCCAT
16741 CTCCCAACTT TCCAACCCAT ATTCCACATT AATCCCTTCC ACCACCATGC AACACTAGGT
16801 AGGAGAGAAG GAAGGTTAGA AGAGAAAGTG GGTATAGATC TATTTAGACT ACTTCCTGCT
16861 GATTAGGGGC AAGTCCAATC GTCATTGTCA GGATACCTCC AACCAGCAAC CAGCAAACCA
16921 GCAAATCAGA AACAGCAAAA GCAGCCAACA AGGCAGCACT AACCAGCAGG ATTGGGGTCG
16981 GTAGCGTGGG AGCAGTCACT ACTGGTCTTC TCATGGCTTT GGCATTAATA CTCTCTCAAG
17041 AAATTCGGTA ATTTTTTCCC CACCACCTGA AATTCGGTAA TTTTAAATGC AAATATCTA
17101 CAGCTGGCAA AAATCACATC TCTCCTAGAG CACAAGACAA ATCATAGTTA CTGGCTATTT
17161 GCAATCTGAA GCATCTCAAT ATCCCACACC TGGGATTAAA ACAAAAACAT ATTCACATCA
17221 CATACTGTT TTTTTTTTCC AATTTTTTAT TAGGTATTTT CTTTATTTAC ATTTCAAATG
17281 CTATCCCGAA AGTCCCCTAT ACCCTCCAC CTCCCTGCTC CCCTACACAC CCCTCCAC
17341 TTTTGTACCC TGGAGTTCCC CGGTACTGGG GCATATAAAG TTTGCAAGAC CAAGGGGCCT
17401 CTCTTCCAG TGATGGCCGA CTAAGCCATC TTCTGCTACA TATGCAGATA GAGACACGAG
17461 CTCTGGGGGT ACTAGTTAGT TCATATTGTT GTTCCACCTA TAGGGTCGCA GACCCCTTCA
17521 GCTCCTTGGG TACTTTGTCT AGCTCCTCCA CTGGGGGCTC TGTGTTTTAT CTAATAGATG
17581 ACTGTGAGCA TCCACTTCTG TATTTGACAG GCACTGGCCT AGCGTCACAT GAGCCAGCTA
17641 TATCAGGGTC CTTTCAGCAA AACCTTGCTG GCATGTGCAA TAGTGTCTGC GTTTGGTGGT
17701 TGATTATGGG ATGGATCCAC TAGTTCTAGA GC

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